

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:46:47 ; Search time 39 Seconds

(without alignments)
2470.284 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858
Sequence: 1 MSFLGLLVTSALAGRGRT.....DVALEHHECDVCGRSTGG 345

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEM_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEM_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEM_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEM_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10_NEM_PUB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US60_NEM_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	345	9	US-09-818-943-1
2	1858	100.0	345	9	US-09-852-209A-3
3	1858	100.0	345	12	US-10-439-337A-3
4	1858	100.0	345	12	US-10-303-997B-3
5	1858	100.0	345	13	US-10-086-623-32
6	1858	100.0	345	14	US-10-260-539-32
7	1858	100.0	345	14	US-10-131-600-3
8	1851	99.6	345	9	US-09-823-033-2
9	1851	99.6	345	9	US-09-923-995-4
10	1851	99.6	345	9	US-09-795-006A-149
11	1851	99.6	345	9	US-09-978-285A-488
12	1851	99.6	345	9	US-09-978-697-488
13	1851	99.6	345	9	US-09-978-192A-488
14	1851	99.6	345	9	US-09-999-832A-488
15	1851	99.6	345	10	US-09-978-189-488

16	1851	99.6	345	10	US-09-796-753-6
17	1851	99.6	345	10	US-09-978-608A-488
18	1851	99.6	345	10	US-09-978-585A-488
19	1851	99.6	345	10	US-09-978-191A-488
20	1851	99.6	345	10	US-09-978-403A-488
21	1851	99.6	345	10	US-09-978-564A-488
22	1851	99.6	345	10	US-09-999-833A-488
23	1851	99.6	345	10	US-09-981-915A-488
24	1851	99.6	345	10	US-09-978-824-488
25	1851	99.6	345	10	US-09-918-585A-488
26	1851	99.6	345	10	US-09-978-423A-488
27	1851	99.6	345	10	US-09-978-193A-488
28	1851	99.6	345	10	US-09-999-830A-488
29	1851	99.6	345	10	US-09-978-157A-488
30	1851	99.6	345	10	US-09-978-187A-488
31	1851	99.6	345	10	US-09-978-643A-488
32	1851	99.6	345	10	US-09-978-375A-488
33	1851	99.6	345	10	US-09-978-298A-488
34	1851	99.6	345	10	US-09-978-188A-488
35	1851	99.6	345	10	US-09-978-681A-488
36	1851	99.6	345	10	US-09-978-194A-488
37	1851	99.6	345	10	US-09-999-829A-488
38	1851	99.6	345	10	US-09-978-829A-488
39	1851	99.6	345	10	US-09-978-544A-488
40	1851	99.6	345	10	US-09-978-665A-488
41	1851	99.6	345	10	US-09-978-802A-488
42	1851	99.6	345	11	US-09-876-813-33
43	1851	99.6	345	12	US-10-147-493-286
44	1851	99.6	345	12	US-10-164-749A-488
45	1851	99.6	345	12	US-10-145-127-286

ALIGNMENTS

RESULT 1
US-09-818-943-1
Sequence 1, Application US/09818943
Patent No. US20020049987A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: LI, Xuri
APPLICANT: PONTEN, Annika
APPLICANT: MASE, Karin
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH
FILE REFERENCE: 1064/48487
CURRENT APPLICATION NUMBER: US/09/818, 943
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/192,507
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-818-943-1
Query Match
Best Local Similarity 100.0%; Score 1858; DB 9; Length 345;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSFLGLLVTSALAGRGRTQAESNLSKPFQSNKQNGVQDPQHRITVSTNGSIHS 60
Db 1 MSFLGLLVTSALAGRGRTQAESNLSKPFQSNKQNGVQDPQHRITVSTNGSIHS 60
OY 61 PRPHITVPRNTVTLVWRLVAEENWVLTDTDERFGLEDPEDDICTKYFVEEYPSDGTIL 120
Db 61 PRPHITVPRNTVTLVWRLVAEENWVLTDTDERFGLEDPEDDICTKYFVEEYPSDGTIL 120
OY 121 GRWGSSTVPGKQSKNQIRIRFVSDYFPPSEGFCHINIVWPQTEAVSPVLPPSA 180

Db 121 GRWGSCTVPGKQISKNQIRIRFVSDYFPESEBGFCHINIVMPQFTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDNL 240
Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDNL 240
QY 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
Db 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
QY 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
Db 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345

RESULT 2

US-09-852-209A-3
Sequence 3, Application US/09852209A
Patent No. US20020164687A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: TUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christel
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-209A-3

Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 6,8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSKRFQSSNKEQNGVDPQHERITTVSTNGSIHS 60
Db 1 MSLEGLLVTSALAGRGTOAESNLSKRFQSSNKEQNGVDPQHERITTVSTNGSIHS 60
QY 61 PREPHYPRNTVLMRLVAVENVMWQLTFDERFGLEDDEDICCKDFVVEBPSDGTLL 120
Db 61 PREPHYPRNTVLMRLVAVENVMWQLTFDERFGLEDDEDICCKDFVVEBPSDGTLL 120
QY 121 GRWGSCTVPGKQISKNQIRIRFVSDYFPESEBGFCHINIVMPQFTEAVSPSVLPSPA 180
Db 121 GRWGSCTVPGKQISKNQIRIRFVSDYFPESEBGFCHINIVMPQFTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDNL 240
Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDNL 240

QY 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
Db 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
QY 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
Db 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345

RESULT 3

US-10-439-337A-3
Sequence 3, Application US/10439337A
Publication No. US20040053837A1
GENERAL INFORMATION:
APPLICANT: Li, Xuri
APPLICANT: ERIKSSON, Ulf
APPLICANT: CARMELIET, Peter
TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND
FILE REFERENCE: 029065, 44740C4
CURRENT APPLICATION NUMBER: US/10/439,337A
CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 10/303,997
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 60/102,461
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: US 60/108,109
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: US 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: US 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-439-337A-3

Query Match 100.0%; Score 1858; DB 12; Length 345;
Best Local Similarity 100.0%; Pred. No. 6,8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSKRFQSSNKEQNGVDPQHERITTVSTNGSIHS 60
Db 1 MSLEGLLVTSALAGRGTOAESNLSKRFQSSNKEQNGVDPQHERITTVSTNGSIHS 60
QY 61 PREPHYPRNTVLMRLVAVENVMWQLTFDERFGLEDDEDICCKDFVVEBPSDGTLL 120
Db 61 PREPHYPRNTVLMRLVAVENVMWQLTFDERFGLEDDEDICCKDFVVEBPSDGTLL 120
QY 121 GRWGSCTVPGKQISKNQIRIRFVSDYFPESEBGFCHINIVMPQFTEAVSPSVLPSPA 180
Db 121 GRWGSCTVPGKQISKNQIRIRFVSDYFPESEBGFCHINIVMPQFTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDNL 240
Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDNL 240
QY 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
Db 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
QY 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
Db 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345

Db 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALBHHBECDCVCRGSTG 345

RESULT 4

```

US-10-303-997B-3
; Sequence 3, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.4474003
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-303-997B-3

Query Match      100.0%; Score 1858; DB 12; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLFGLLVTSALAGRRGTQAESNLSSKQFSSNKEONGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLLFGLLVTSALAGRRGTQAESNLSSKQFSSNKEONGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHITYPRNTVLVWRLVAABENWMIQITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
DB 61 PRPHITYPRNTVLVWRLVAABENWMIQITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
QY 121 GRWGSSTVPGKQISKNOQIRIRFVSDYFSPBEGFCIHNYIWPQTEAVSPSVLPSPA 180
DB 121 GRWGSSTVPGKQISKNOQIRIRFVSDYFSPBEGFCIHNYIWPQTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTWQLGKAFVFGKSRVVDNL 240
DB 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTWQLGKAFVFGKSRVVDNL 240
QY 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIIPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIIPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALBHHBECDCVCRGSTG 345
DB 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALBHHBECDCVCRGSTG 345

```

RESULT 5

```

US-10-086-623-32
; Sequence 32, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf

```

APPLICANT: AASE, Karin

APPLICANT: LI, Xuri

APPLICANT: PONTEN, Annica

APPLICANT: UTTELA, Maiko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES 1

FILE REFERENCE: 1064/448332

CURRENT APPLICATION NUMBER: US/10/086,623

PRIOR FILING DATE: 2000-03-04

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 60/113,997

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: US 60/150,604

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: US 60/157,108

PRIOR FILING DATE: 1999-10-04

PRIOR APPLICATION NUMBER: US 60/157,756

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 09/691,200

PRIOR FILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: misc feature

OTHER INFORMATION: Amino acid sequence for PDGF-C

US-10-086-623-32

Query Match 100.0%; Score 1858; DB 13; Length 345;

Best Local Similarity 100.0%; Pred. No. 6.8e-179;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSLLFGLLVTSALAGRRGTQAESNLSSKQFSSNKEONGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLLFGLLVTSALAGRRGTQAESNLSSKQFSSNKEONGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHITYPRNTVLVWRLVAABENWMIQITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
DB 61 PRPHITYPRNTVLVWRLVAABENWMIQITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
QY 121 GRWGSSTVPGKQISKNOQIRIRFVSDYFSPBEGFCIHNYIWPQTEAVSPSVLPSPA 180
DB 121 GRWGSSTVPGKQISKNOQIRIRFVSDYFSPBEGFCIHNYIWPQTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTWQLGKAFVFGKSRVVDNL 240
DB 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTWQLGKAFVFGKSRVVDNL 240
QY 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIIPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIIPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALBHHBECDCVCRGSTG 345
DB 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALBHHBECDCVCRGSTG 345

```

RESULT 6

```

US-10-260-539-32
; Sequence 32, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri

```

```

; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32

```

```

Query Match      100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 6,8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERITITVSTNSIHS 60
DB 1 MSIFGLLVTSLAAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERITITVSTNSIHS 60
QY 61 PREPHTYPRNTLVWRLVAEENWVQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTLVWRLVAEENWVQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180
QY 181 LPDLNNATITAFSTEDLIRYLEPFRWQDLIEDLYRPTWQLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITAFSTEDLIRYLEPFRWQDLIEDLYRPTWQLLGKAFVGRKSRVVDNL 240
QY 241 LITEEVALYSCPTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNHCNCCQCVPSK 300
DB 241 LITEEVALYSCPTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNHCNCCQCVPSK 300
QY 301 VTKKYHEVLQLRPKTVGRGLHKSLLTDVALEHHEBCDCVCRGSTGG 345
DB 301 VTKKYHEVLQLRPKTVGRGLHKSLLTDVALEHHEBCDCVCRGSTGG 345

```

```

RESULT 7
US-10-131-600-3
; Sequence 3, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: MASE, Karin
; APPLICANT: LEE, Xuri

```

```

; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: THEREFOR, AND USES THEREOF
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-3

```

```

Query Match      100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 6,8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERITITVSTNSIHS 60
DB 1 MSIFGLLVTSLAAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERITITVSTNSIHS 60
QY 61 PREPHTYPRNTLVWRLVAEENWVQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTLVWRLVAEENWVQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180
QY 181 LPDLNNATITAFSTEDLIRYLEPFRWQDLIEDLYRPTWQLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITAFSTEDLIRYLEPFRWQDLIEDLYRPTWQLLGKAFVGRKSRVVDNL 240
QY 241 LITEEVALYSCPTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNHCNCCQCVPSK 300
DB 241 LITEEVALYSCPTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNHCNCCQCVPSK 300
QY 301 VTKKYHEVLQLRPKTVGRGLHKSLLTDVALEHHEBCDCVCRGSTGG 345
DB 301 VTKKYHEVLQLRPKTVGRGLHKSLLTDVALEHHEBCDCVCRGSTGG 345

```

```

RESULT 8
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. US2002004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5

```


SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60
DB 1 MSFLGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHYPRNTVTVLWRLVAEENWVIOQLTDFERFGLDEPDDICKYDVEVEEBSDDGTL 120
DB 61 PRPHYPRNTVTVLWRLVAEENWVIOQLTDFERFGLDEPDDICKYDVEVEEBSDDGTL 120
QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFPSEBPGFCIHNYIWMPOFTEAVSPSVLPESA 180
DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFPSEBPGFCIHNYIWMPOFTEAVSPSVLPESA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240
QY 241 LTBVRLVYSCTPRNFVSISIRELKRDTDTIIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
DB 241 LTBVRLVYSCTPRNFVSISIRELKRDTDTIIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLOLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345
DB 301 VTKKYHEVLOLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345

RESULT 9
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60
DB 1 MSFLGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHYPRNTVTVLWRLVAEENWVIOQLTDFERFGLDEPDDICKYDVEVEEBSDDGTL 120
DB 61 PRPHYPRNTVTVLWRLVAEENWVIOQLTDFERFGLDEPDDICKYDVEVEEBSDDGTL 120
QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFPSEBPGFCIHNYIWMPOFTEAVSPSVLPESA 180
DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFPSEBPGFCIHNYIWMPOFTEAVSPSVLPESA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240

DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240
QY 241 LTBVRLVYSCTPRNFVSISIRELKRDTDTIIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
DB 241 LTBVRLVYSCTPRNFVSISIRELKRDTDTIIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLOLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345
DB 301 VTKKYHEVLOLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345

RESULT 10
US-09-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Allcalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-149

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60
DB 1 MSFLGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHYPRNTVTVLWRLVAEENWVIOQLTDFERFGLDEPDDICKYDVEVEEBSDDGTL 120
DB 61 PRPHYPRNTVTVLWRLVAEENWVIOQLTDFERFGLDEPDDICKYDVEVEEBSDDGTL 120
QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFPSEBPGFCIHNYIWMPOFTEAVSPSVLPESA 180
DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFPSEBPGFCIHNYIWMPOFTEAVSPSVLPESA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNTL 240
QY 241 LTBVRLVYSCTPRNFVSISIRELKRDTDTIIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
DB 241 LTBVRLVYSCTPRNFVSISIRELKRDTDTIIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLOLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345
DB 301 VTKKYHEVLOLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345

RESULT 11
US-09-978-295A-488
; Sequence 488, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyere, Luc

APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Pong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivac J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079669
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920

PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083332
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3, 5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 MSLFGLLVTSALAGORRGTOAESNLSSKFOFSSNKEQNGVDDPQHERIITVSTNGSIHS 60
1 MSLFGLLVTSALAGORRGTOAESNLSSKFOFSSNKEQNGVDDPQHERIITVSTNGSIHS 60
61 PRPPTTYRNTVTVLWRLVAEENWMIQLTPDRFLEPDEDDICRYDVEVEEPEBDGTL 120
61 PRPPTTYRNTVTVLWRLVAEENWMIQLTPDRFLEPDEDDICRYDVEVEEPEBDGTL 120
121 GRWGCGTVPGKQISKGNQIRIRFVSDVEYFSEPGFCHYNIWMPQFTEAVSPVLPPSA 180
121 GRWGCGTVPGKQISKGNQIRIRFVSDVEYFSEPGFCHYNIWMPQFTEAVSPVLPPSA 180
121 GRWGCGTVPGKQISKGNQIRIRFVSDVEYFSEPGFCHYNIWMPQFTEAVSPVLPPSA 180
181 LPLDLINNAITAFSTLEDLIRYLBEPWQLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
181 LPLDLINNAITAFSTLEDLIRYLBEPWQLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
181 LPLDLINNAITAFSTLEDLIRYLBEPWQLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
241 LTEEVRKLSCTPRNSVSIRBELKRTDTTFWPGCLLVRCGNGACCLHNCNECCQVSK 300
241 LTEEVRKLSCTPRNSVSIRBELKRTDTTFWPGCLLVRCGNGACCLHNCNECCQVSK 300
301 VTKKYHEVTLQRPKTGVGLHKSITDVALHNEECDCVCRSGTGG 345

DB 301 VTKKYHEVTLQRPKTGVGLHKSITDVALHNEECDCVCRSGTGG 345
RESULT 12
US-09-978-697-488
Sequence 488, Application US/0978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978, 697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25

;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079920
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/079923
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080334
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081952
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082569
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392

;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083500
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGRRGTQAESNLSKPFSSNKEQNGVODPOHERITVSTNGSIHS 60
DB 1 MSIFGLLVTSALAGRRGTQAESNLSKPFSSNKEQNGVODPOHERITVSTNGSIHS 60
QY 61 PRPHPTYPNTVYVWLVVVEENWVQLTFDERFGLEDEDDICXKDFVVEEPPSGTLL 120
DB 61 PRPHPTYPNTVYVWLVVVEENWVQLTFDERFGLEDEDDICXKDFVVEEPPSGTLL 120

QY 121 GRWGSGTVGSGKQISKQNIIRFVSDYFSPSPGCIHYNIVMPQFTEAVSPSULPSPA 180
Db 121 GRWGSGTVGSGKQISKQNIIRFVSDYFSPSPGCIHYNIVMPQFTEAVSPSULPSPA 180
QY 181 LPDLNNATATFSTLEDLIRYLEPERWQDLEDLIRPTWQLGKAFVGRKSRVVDLNT 240
Db 181 LPDLNNATATFSTLEDLIRYLEPERWQDLEDLIRPTWQLGKAFVGRKSRVVDLNT 240
QY 241 LTRVRLYSCTRPRNSYSIRELKRDTDTIFPFGCLLYKRCGCGNACCLHNCNQCVPSPK 300
Db 241 LTRVRLYSCTRPRNSYSIRELKRDTDTIFPFGCLLYKRCGCGNACCLHNCNQCVPSPK 300
QY 301 VTKKHVQLQRPRTGVRGLHKSJLDVALHHEBCDCVCRSGTGG 345
Db 301 VTKKHVQLQRPRTGVRGLHKSJLDVALHHEBCDCVCRSGTGG 345

RESULT 13
US-09-978-192A-488
Sequence 488, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085333
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085669
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3,5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSIFGLLVTSALAGRRGTQAEBSNLSKPFQSSNKEQNGVDPQHERIITVSTNSIS 60
DB 1 MSIFGLLVTSALAGRRGTQAEBSNLSKPFQSSNKEQNGVDPQHERIITVSTNSIS 60
QY 61 PREPHTYPRNTVYVWVLVVEENWVITQTFDERFGLEDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVYVWVLVVEENWVITQTFDERFGLEDEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPGKQISKQNOIRIRFVSDEXFSPBPGFCIHNYIMPOFTEAVSPSVLP 180
DB 121 GRWCGSGTVPGKQISKQNOIRIRFVSDEXFSPBPGFCIHNYIMPOFTEAVSPSVLP 180
QY 181 LPDLNNATITASTIEDIRILEPFRMOLDIEDLYRFTWOLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITASTIEDIRILEPFRMOLDIEDLYRFTWOLGKAFVGRKSRVVDNL 240
QY 241 LFEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKCGGACCLHNCNECQCVPSK 300
DB 241 LFEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKCGGACCLHNCNECQCVPSK 300
QY 301 VTKYHEVILQRPKTGVRLKSLTDVALEHHEBCDVCRGSTGG 345
DB 301 VTKYHEVILQRPKTGVRLKSLTDVALEHHEBCDVCRGSTGG 345
RESULT 14
US-09-999-832A-488
Sequence 488, Application US/0999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurley, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thmas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03

[illegible]

PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081819
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081952
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082566
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082804
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082700
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082766
PRIOR FILING DATE:	1998-04-23
PRIOR APPLICATION NUMBER:	60/083336
PRIOR FILING DATE:	1998-04-27
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083392
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083495
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083454
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083496
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083499
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083558
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083500
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083742
PRIOR FILING DATE:	1998-04-30
PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084441
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084627
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084588
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085338
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085323
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15

```
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3,5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSNNKQNGVDPQHERITITVSTNGSIHS 60
DB 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSNNKQNGVDPQHERITITVSTNGSIHS 60
QY 61 PRPHYPRNTVLYWRLVAEENWVIOQLTDERFGLEDPEDDI CKXDFVEEPPSDGTL 120
DB 61 PRPHYPRNTVLYWRLVAEENWVIOQLTDERFGLEDPEDDI CKXDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQISKQNOIRIRFVSDEYFSEBPGFCIHNYIVMPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKQISKQNOIRIRFVSDEYFSEBPGFCIHNYIVMPQFTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTLEDLIRYEPERWQDLEDLVRPTQGLGKAFVFRKSRVVDLNL 240
DB 181 LPDLNNATTAFTSTLEDLIRYEPERWQDLEDLVRPTQGLGKAFVFRKSRVVDLNL 240
QY 241 LTEEVRYSCTPNFVSISIEELKRTTTFMPGGLVYKRCGNCACCLHNCNCCQCVPSK 300
DB 241 LTEEVRYSCTPNFVSISIEELKRTTTFMPGGLVYKRCGNCACCLHNCNCCQCVPSK 300
QY 301 VTKKYHEVQLRPRTGVRLGKSLTDVALHHEECDCVCGSGTGG 345
DB 301 VTKKYHEVQLRPRTGVRLGKSLTDVALHHEECDCVCGSGTGG 345

RESULT 15
US-09-978-189-488
/ Sequence 488, Application US/09978189
/ Publication No. US20030004102A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, V. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tuma, Daniel
```

```
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C7
/ CURRENT APPLICATION NUMBER: US/09/978,189
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 60/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077641
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
/ PRIOR APPLICATION NUMBER: 60/078004
/ PRIOR FILING DATE: 1998-03-13
/ PRIOR APPLICATION NUMBER: 60/078886
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078936
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078939
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079664
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079663
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079786
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079920
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/079923
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/080105
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080107
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080165
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080194
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080327
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080328
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080333
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080334
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/081070
/ PRIOR FILING DATE: 1998-04-08
```


PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081819
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081952
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083500
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/083666
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085562
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 10; Length 345;
 Best Local Similarity 99.4%; Pred. No. 3.5e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 MSLEGLLLTASLAGORGTQAESNLSSKPFSSNKEONGVQDPQHRITVSTNGSIHS 60
 1 MSLEGLLLTASLAGORGTQAESNLSSKPFSSNKEONGVQDPQHRITVSTNGSIHS 60
 61 PRPHYTPRNTVLMRLVAEENVMQLTFDERFGLEDPEDDICKYDFVEEESPSDGTIL 120
 61 PRPHYTPRNTVLMRLVAEENVMQLTFDERFGLEDPEDDICKYDFVEEESPSDGTIL 120
 121 GRWCGSGTVPGKQSKGNQIRIRFVSDEYPPSEGFCHININWPOTEAVSPSVLPSSA 180
 121 GRWCGSGTVPGKQSKGNQIRIRFVSDEYPPSEGFCHININWPOTEAVSPSVLPSSA 180
 181 LPDLNNATTAFTLDELRLYLEPERMQLDELTPYPTQLKAKAVFGKRSVVDLNL 240
 181 LPDLNNATTAFTLDELRLYLEPERMQLDELTPYPTQLKAKAVFGKRSVVDLNL 240
 241 LTBVRLYSCTPRNFSYSIREBELKRTDTIFMPGCLVRCGNCACCLHNCNECQCVPSK 300
 241 LTBVRLYSCTPRNFSYSIREBELKRTDTIFMPGCLVRCGNCACCLHNCNECQCVPSK 300
 301 VTKKYHEVLQRPKTVGRGLHKSITDVALBHEBECDCVCRSGTSG 345
 301 VTKKYHEVLQRPKTVGRGLHKSITDVALBHEBECDCVCRSGTSG 345

Search completed: May 27, 2004, 15:56:26
 Job time : 41 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:37:31 ; Search time 51 Seconds
(without alignments)
1911.351 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1 MSLEGLLVTSALAGRGRT.....DVLEHHECDVCGRSGTGG 345

Sequence: 1 MSLEGLLVTSALAGRGRT.....DVLEHHECDVCGRSGTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: _geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	345	3	AAV84557 Amino act
2	1858	100.0	345	5	AAE13212 Human pla
3	1851	99.6	345	2	AAE14766 Human PRO
4	1851	99.6	345	2	AAV30023 Human vas
5	1851	99.6	345	2	AAV33679 Human VEG
6	1851	99.6	345	3	AAV33414 Human PRO
7	1851	99.6	345	3	AAV19578 Human PRO
8	1851	99.6	345	3	AAV10651 Human VEG
9	1851	99.6	345	3	AAV10633 Human RAC
10	1851	99.6	345	3	AAV10650 Human 990
11	1851	99.6	345	3	AAV10635 Human VEG
12	1851	99.6	345	3	AAV10644 Human VEG
13	1851	99.6	345	3	AAV44322 Human PRO
14	1851	99.6	345	3	AAV24412 Human PRO
15	1851	99.6	345	3	AAV59285 Bone moirp
16	1851	99.6	345	3	AAV96858 Human gro
17	1851	99.6	345	3	AAV48657 Human zve
18	1851	99.6	345	3	AAV01419 Human TAN
19	1851	99.6	345	3	AAV24250 Human pla
20	1851	99.6	345	4	AAV02649 Human lrp8
21	1851	99.6	345	4	AAV12314 Human PRO
22	1851	99.6	345	4	AAV53074 Human ang
23	1851	99.6	345	4	AAV74028 Human VEG
24	1851	99.6	345	4	AAV65603 Human zve
25	1851	99.6	345	4	AAV08465 Polypepti

26	1851	99.6	345	4	AAV50980 Human PRO
27	1851	99.6	345	4	AAV49895 Human PRO
28	1851	99.6	345	4	AAV00997 Human zve
29	1851	99.6	345	5	AAV79984 Human vas
30	1851	99.6	345	5	AAV92889 Human VEG
31	1851	99.6	345	5	AAV47889 Human zve
32	1851	99.6	345	5	AAV81331 Human VEG
33	1851	99.6	345	5	AAV76684 Human zve
34	1851	99.6	345	6	AAV17758 Human hum
35	1851	99.6	345	6	AAV72434 Human zve
36	1851	99.6	345	6	AAV025268 Novel hum
37	1851	99.6	345	6	AAV81012 Human PRO
38	1851	99.6	345	6	AAV72274 Human PRO
39	1851	99.6	345	6	AAV66712 Human PRO
40	1851	99.6	345	6	AAV84954 Human sec
41	1851	99.6	345	6	AAV72132 Human vas
42	1851	99.6	345	6	AAV59793 Human sec
43	1851	99.6	345	6	AAV61152 Human PRO
44	1851	99.6	345	6	AAV024983 Human sec
45	1851	99.6	345	6	AAV76393 Human gro

ALIGNMENTS

RESULT 1	AAV84557	standard; protein; 345 AA.
ID	AAV84557	
AC	AAV84557	
DT	25-JUL-2000	(first entry)
DE	Amino acid sequence of platelet-derived growth factor C (PDGF-C).	
XX	Platelet-derived growth factor C; PDGF-C; cell proliferation;	
XX	growth factor; heparin; connective tissue; wound healing; VEGF-F;	
XX	fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;	
XX	choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;	
XX	lung carcinoma; erythroleukemia; tissue remodeling.	
OS	Homo sapiens.	
XX		
XX	WO200018212-A2.	
XX		
XX	06-APR-2000.	
XX		
XX	30-SEP-1999; 99WO-US022668.	
XX		
XX	30-SEP-1998; 98US-0102461P.	
XX	12-NOV-1998; 98US-0108109P.	
XX	03-DEC-1998; 98US-0110749P.	
XX	18-DEC-1998; 98US-0113002P.	
XX	21-MAY-1999; 99US-0135426P.	
XX	15-JUL-1999; 99US-0144022P.	
XX		
XX	(LUDWIG INST CANCER RES.	
XX	(UTHE-) UNIV HELSINKI LICENSING LTD.	
XX		
XX	Eriksson U, Aase K, Ponten A, Uuteia M, Alltalo K;	
XX	Oestman A, Heldin C, Betsholtz C;	
XX		
XX	WPI; 2000-292954/25.	
XX	N-PSDB; AAA12523.	
XX		
XX	Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,	
XX	differentiation, growth and motility of cells expressing the PDGF-C	
XX	receptor.	
XX		
XX	Claim 27; Fig 2; 135pp; English.	
XX		
XX	The present sequence represents human platelet-derived growth factor C	
XX	(PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the	

CC ability to stimulate and enhance proliferation or differentiation, and/or
CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C
CC polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor and
CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used
CC for stimulating connective tissue or wound healing. The PDGF-C
CC polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumor growth of a tumor
CC expressing PDGF-C in a mammal. Specific types of human tumors, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of PDGF-
CC C. PDGF-C antagonists can also be used to inhibit tissue remodeling
CC during invasion of tumor cells into a normal population of cells.
CC Antagonists can also be used to treat fibrotic conditions, especially
CC found in the lung, kidney or liver

CC Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.3e-179; Mismatches 0; Gaps 0;
Matches 345; Conservative 0; Indels 0;

QY 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHPTPVNTVYVWRLVAVENWVLTQFDERFGLEDDEDDICXDFVEVEPSDGTIL 120
DB 61 PRPHPTPVNTVYVWRLVAVENWVLTQFDERFGLEDDEDDICXDFVEVEPSDGTIL 120
QY 121 GRWGSSTGVGKQISGKQIRIRFVSDPEPSPGCIHYNIVMPQFTAVSPSVLPESA 180
DB 121 GRWGSSTGVGKQISGKQIRIRFVSDPEPSPGCIHYNIVMPQFTAVSPSVLPESA 180
QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LTBEPVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
DB 241 LTBEPVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
QY 301 VTKKHVAVQLRPKTGVRLGHSKSLTDVALHHEBCDCVCRGSTGG 345
DB 301 VTKKHVAVQLRPKTGVRLGHSKSLTDVALHHEBCDCVCRGSTGG 345

RESULT 2
AAE13212
ID AAE13212 standard; protein; 345 AA.

XX AAE13212;
AC
XX
DT 12-FEB-2002 (first entry)
XX
DE Human platelet-derived growth factor (PDGF-C) protein.
XX
KW Human; transgenic animal; platelet derived growth factor C; PDGF-C;
XX cardiac hypertrophy; fibrosis.
XX
OS Homo sapiens.
XX
PN MO200172132-A1.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001MO-US009855.
XX
PR 28-MAR-2000; 2000US-0192507P.
XX

PA (LUDW-) LUDWIG INST CANCER RES.

PI Eriksson U, Li X, Ponten A, Aase K, Li H;

DR WPI; 2002-010700/01.

PT A transgenic animal over-expressing platelet derived growth factor C is
PT useful to study and find therapy for disease associated with PDGF-C over-
PT expression, including cardiac hypertrophy and fibrosis.

PS Disclosure, Page 40-42; 48pp; English.

CC The patent discloses a method for producing a transgenic, non-human
CC animal over-expressing a platelet derived growth factor C (PDGF-C), or
CC its functional fragment or analogue. The method involves introducing a
CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the
CC cell into a non-human animal and allowing the cell to develop into a
CC transgenic, non-human animal. The transgenic animal is useful as a model
CC to study disease states characterised by over-expression of PDGF-C and to
CC find therapy for those diseases, particularly hypertrophy and fibrosis in
CC various organs including the heart. The present sequence is PDGF-C
CC protein from human

SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.3e-179; Mismatches 0; Gaps 0;
Matches 345; Conservative 0; Indels 0;

QY 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHPTPVNTVYVWRLVAVENWVLTQFDERFGLEDDEDDICXDFVEVEPSDGTIL 120
DB 61 PRPHPTPVNTVYVWRLVAVENWVLTQFDERFGLEDDEDDICXDFVEVEPSDGTIL 120
QY 121 GRWGSSTGVGKQISGKQIRIRFVSDPEPSPGCIHYNIVMPQFTAVSPSVLPESA 180
DB 121 GRWGSSTGVGKQISGKQIRIRFVSDPEPSPGCIHYNIVMPQFTAVSPSVLPESA 180
QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LTBEPVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
DB 241 LTBEPVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
QY 301 VTKKHVAVQLRPKTGVRLGHSKSLTDVALHHEBCDCVCRGSTGG 345
DB 301 VTKKHVAVQLRPKTGVRLGHSKSLTDVALHHEBCDCVCRGSTGG 345

RESULT 3
AA41766
ID AA41766 standard; protein; 345 AA.

XX AA41766;
AC
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO200 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO946281-A2.
XX
PD 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.
PF
XX 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077643P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079299P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080344P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083549P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084419P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.

PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086033P.
PR 22-MAY-1998; 98US-0086352P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086430P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.

XX (GETH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI, 1999-551358/46.

DR N-PSDB; AAZ34296.

XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.

PS Claim 12; Fig 207; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ3891 to AAZ34338, and AAZ41685 to
CC AAZ41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention

SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 2; Length 345;

Best Local Similarity 99.4%; Pred. No. 2,2e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSFLGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60
QY PRPHPTVPMNTVLVWRLVAABENWVIOITDERGLEDPEDDICKYFVEVEEBSDDGTL 120
DB PRPHPTVPMNTVLVWRLVAABENWVIOITDERGLEDPEDDICKYFVEVEEBSDDGTL 120
QY 61 PRPHPTVPMNTVLVWRLVAABENWVIOITDERGLEDPEDDICKYFVEVEEBSDDGTL 120
DB 61 PRPHPTVPMNTVLVWRLVAABENWVIOITDERGLEDPEDDICKYFVEVEEBSDDGTL 120
QY 121 GRWCGSTVPGKOISKNGQIRIRFVSDEYPSSEBGFCHYNIWVPQTEAVSPSLPPSA 180
DB 121 GRWCGSTVPGKOISKNGQIRIRFVSDEYPSSEBGFCHYNIWVPQTEAVSPSLPPSA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLELYRPTMQLGKAVVFGKRSVVDLNT 240
DB 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLELYRPTMQLGKAVVFGKRSVVDLNT 240
QY 241 LTBVRLYSCPTPRFVSISIREELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
DB 241 LTBVRLYSCPTPRFVSISIREELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLOLRPTGVRGLHKSLTDVLEHHEBCDCVCRGSTGG 345
DB 301 VTKKYHEVLOLRPTGVRGLHKSLTDVLEHHEBCDCVCRGSTGG 345

RESULT 4

AAV30023
ID AAV30023 standard; protein; 345 AA.

XX
XX AAV30023;

DT 11-OCT-1999 (first entry)

XX Human vascular endothelial growth factor related protein.

DE Vascular endothelial growth factor related protein; VEGF-R protein;

KW tissue growth inhibition; tumour growth; cancer; tissue growth;

KW angiogenesis; coronary artery blockage.

XX Homo sapiens.

PN MO993671-A1.

PD 29-JUL-1999.

XX 26-JAN-1999; 99WO-US001574.

XX 27-JAN-1998; 98US-0072635P.

PR 05-JUN-1998; 98US-0088089P.

PR 24-JUN-1998; 98US-0090544P.

PR 31-AUG-1998; 98US-0098548P.

XX (ELIL) LILLY & CO ELI.

XX Dou S. Na S. Song HY;

XX WPI; 1999-458680/38.

DR N-PSDB; AAX6352.

PT A vascular endothelial growth factor related protein and related

XX polynucleotide, useful for identifying antagonists and binding compounds.

XX Claim 1; Page 56-58; 62pp; English.

XX The present sequence represents a vascular endothelial growth factor

CC related (VEGF-R) protein. VEGF-R can be used in assays to identify

CC compounds that bind to it or that antagonize its activity. VEGF-R

CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting

CC tissue growth. This is useful for inhibiting tumour growth and for

CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,

CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding

CC sequence can be used for the recombinant production of the VEGF-R protein

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 2; Length 345;

Best Local Similarity 99.4%; Pred. No. 2.2e-178;

Matches 345; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGRGRTQAESNLSSKQFSSNKQNGVDPQHERITTVTNGSIHS 60

DB 1 MSIFGLLVTSALAGRGRTQAESNLSSKQFSSNKQNGVDPQHERITTVTNGSIHS 60

QY 61 PRPHPTVPRNTVAVLRVAEENWVITQITDERPGLDEPDDICTYDFVEEPPSDGTL 120

DB 61 PRPHPTVPRNTVAVLRVAEENWVITQITDERPGLDEPDDICTYDFVEEPPSDGTL 120

QY 121 GRGCGSGTVGKQISKGNQIRIRFVSDEYSPSPGFCIHNYIMPOQTEVSSVLPSPA 180

DB 121 GRGCGSGTVGKQISKGNQIRIRFVSDEYSPSPGFCIHNYIMPOQTEVSSVLPSPA 180

QY 181 LPLDLNNATTAFTSTEDLIRYLEPERWQDLVDLYRPTWQLGKAFVFGKRSVVDNL 240

DB 181 LPLDLNNATTAFTSTEDLIRYLEPERWQDLVDLYRPTWQLGKAFVFGKRSVVDNL 240

QY 241 LTRERLYSGCTPPNFSVSIREEIKRTDTITWPGCLLVKRCGACACCLHNCNCCQCPVK 300

DB 241 LTRERLYSGCTPPNFSVSIREEIKRTDTITWPGCLLVKRCGACACCLHNCNCCQCPVK 300

DB 241 LTRERLYSGCTPPNFSVSIREEIKRTDTITWPGCLLVKRCGACACCLHNCNCCQCPVK 300

QY 301 VTKKHEVQLQRPKTVGRGLHKSITDVALFHHBECDVCVRGSGNG 345

DB 301 VTKKHEVQLQRPKTVGRGLHKSITDVALFHHBECDVCVRGSGNG 345

RESULT 5
AAV3679
ID AAV3679 standard; protein; 345 AA.

XX AAV3679;

DT 11-JAN-2000 (first entry)

XX Human VEGF-E protein.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;

KW treatment; cardiovascular disorder; endothelial disorder; therapy;

KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;

KW angiogenic disorder; age-related macular degeneration; vascular disease;

XX neovascularization; tumor; gene mapping.

XX Homo sapiens.

PN MO9947677-A2.

PD 23-SEP-1999.

XX 10-MAR-1999; 99WO-US005190.

XX 17-MAR-1998; 98US-00040220.

PR 02-NOV-1998; 98US-00184216.

XX (GETH) GENENTECH INC.

XX Ferrara N. Kuo SS;

XX WPI; 1999-580306/49.

DR N-PSDB; AAZ23691.

PT New growth factor polypeptide useful for treating cardiovascular or

XX endothelial disorders, e.g. cardiac hypertrophy.

XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular

CC endothelial cell growth factor-E (VEGF-E) polypeptide which has

CC tranquillizer, vulnery and cardiant activity. VEGF-E can be administered

CC therapeutically, especially by expressing encoding polynucleotides, to

CC treat cardiovascular or endothelial disorders in mammals, especially

CC humans. It is useful in wound repair and tissue generation and

CC regeneration, and may especially be used to treat cardiac hypertrophy It

CC can be combined with a carrier in pharmaceutical compositions, which can

CC for antagonists and agonists, and the antagonists administered to treat

CC angiogenic disorders in mammals (especially humans) e.g. cancer or age-

CC related macular degeneration. It can be used to generate antibodies,

CC useful therapeutically as antagonists, as above. The antibodies are also

CC useful to detect VEGF-E polypeptide, especially to diagnose

CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.

CC vascular disease, or neovascularization associated with tumor formation),

CC by contacting the antibody with a tissue sample and detecting formation

CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-

CC E can be used to diagnose cardiovascular and endothelial disorders in

CC mammals, by detecting abnormally high or low VEGF-E gene expression in

CC tissue samples. They can also be used to diagnose a disease or

CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a

CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by

CC detecting a mutation in the VEGF-E-encoding sequence isolated from a

CC sample. They may also be used to produce probes useful to detect related

CC sequences or for gene mapping. This sequence represents the human VEGF-E

CC protein described in the method of the invention

```

XX      Sequence 345 AA;
SQ
Query Match      99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 2.2e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSLLGLLVTALGQRGRTQAESLTSKFPSSKKEQGVDPQHEHITVTSTNGSIHS 60
DB      1 MSLLGLLVTALGQRGRTQAESLTSKFPSSKKEQGVDPQHEHITVTSTNGSIHS 60
QY      61 PRPHPTVPRNTVLVWRLVAVEENWVQLTPDERFGLJEPEDDICKYDFVEYEEPSDGTIL 120
DB      61 PRPHPTVPRNTVLVWRLVAVEENWVQLTPDERFGLJEPEDDICKYDFVEYEEPSDGTIL 120
QY      61 PRPHPTVPRNTVLVWRLVAVEENWVQLTPDERFGLJEPEDDICKYDFVEYEEPSDGTIL 120
DB      61 PRPHPTVPRNTVLVWRLVAVEENWVQLTPDERFGLJEPEDDICKYDFVEYEEPSDGTIL 120
QY      121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSEBPGFCHINYI VMPQTEAVSPSVLPSPA 180
DB      121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSEBPGFCHINYI VMPQTEAVSPSVLPSPA 180
QY      121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSEBPGFCHINYI VMPQTEAVSPSVLPSPA 180
DB      121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSEBPGFCHINYI VMPQTEAVSPSVLPSPA 180
QY      181 LPLDLNNATAPSTLEDLIRYLPBERWQLEDLYRTWQLGKAFVGRKSRVVDINTL 240
DB      181 LPLDLNNATAPSTLEDLIRYLPBERWQLEDLYRTWQLGKAFVGRKSRVVDINTL 240
QY      241 LTBEEVRLVSCTPRRFVSYSIRELKRDTITFMFGCLIVRCGNCACCLHNCNCCQVPSK 300
DB      241 LTBEEVRLVSCTPRRFVSYSIRELKRDTITFMFGCLIVRCGNCACCLHNCNCCQVPSK 300
QY      301 VTKKYHEVQLRPRTGVRGLHKSITDVALHEHBECDCCVCRSGTGG 345
DB      301 VTKKYHEVQLRPRTGVRGLHKSITDVALHEHBECDCCVCRSGTGG 345

```

RESULT 6
AAB33414
ID AAB33414 standard; protein, 345 AA.

AC AAB33414;

DT 29-JAN-2001 (first entry)

DE Human PRO200 protein UNQ174 SEQ ID NO:2.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiac;
 KW dermatological; antidiabetic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neuroprotective;
 KW antidiabetic; hepatic; virucide; antiproliferative; antiallergic;
 KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.

OS Homo sapiens.

XX MO200053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US005841.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99US-0123618P.

XX 12-MAR-1999; 99US-0123957P.

XX 23-MAR-1999; 99US-0125775P.

XX 12-APR-1999; 99US-0128849P.

XX 20-APR-1999; 99WO-US008615.

XX 28-APR-1999; 99US-0131445P.

XX 04-MAY-1999; 99US-0132371P.

```

PR      14-MAY-1999; 99US-0134287P.
PR      02-JUN-1999; 99WO-US012252.
PR      23-JUN-1999; 99US-0141037P.
PR      20-JUL-1999; 99US-0144758P.
PR      26-JUL-1999; 99US-0145698P.
PR      28-JUL-1999; 99US-0146222P.
PR      01-SEP-1999; 99WO-US020111.
PR      08-SEP-1999; 99WO-US020594.
PR      13-SEP-1999; 99WO-US020944.
PR      15-SEP-1999; 99WO-US021090.
PR      15-SEP-1999; 99WO-US021547.
PR      05-OCT-1999; 99WO-US023089.
PR      29-OCT-1999; 99US-0162506P.
PR      29-NOV-1999; 99WO-US028214.
PR      30-NOV-1999; 99WO-US028313.
PR      30-NOV-1999; 99WO-US028409.
PR      01-DEC-1999; 99WO-US028301.
PR      01-DEC-1999; 99WO-US028634.
PR      02-DEC-1999; 99WO-US028551.
PR      02-DEC-1999; 99WO-US028564.
PR      02-DEC-1999; 99WO-US028565.
PR      16-DEC-1999; 99WO-US030095.
PR      20-DEC-1999; 99WO-US030999.
PR      30-DEC-1999; 99WO-US031274.
PR      05-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000277.
PR      06-JAN-2000; 2000WO-US000376.
PR      11-FEB-2000; 2000WO-US003565.
PR      18-FEB-2000; 2000WO-US004341.
PR      18-FEB-2000; 2000WO-US004342.
PR      22-FEB-2000; 2000WO-US004414.

```

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

XX N-PSDB; AAC58579.

XX Claim 33; Fig 2; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

XX be used in the treatment of immune related diseases. The human PRO

XX proteins, anti-PRO antibodies, agonists and antagonists are useful for

XX treating and diagnosing immune related disorders. The disorders are

XX selected from systemic lupus erythematosus, rheumatoid arthritis,

XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

XX immune-mediated renal disease, demyelinating diseases of the central and

XX peripheral nervous systems, hepatobiliary diseases, inflammatory bowel

XX disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune

XX or immune-mediated skin diseases, allergic diseases, immunological

XX diseases of the lung, and transplantation associated diseases including

XX graft rejection and graft-versus-host-disease. AAC58397 to AAC58578

XX represent PCR primers and hybridisation probes used in the isolation of

XX human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477

XX represent human PRO polynucleotide and protein sequences given in the

XX exemplification of the present invention

SO Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60
 DB 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60
 QY 61 PREPHYPRNTVYVWRLVAVEENWVQLTDERFGLEDPEDDICKYDFVEEPPSDGTL 120
 DB 61 PREPHYPRNTVYVWRLVAVEENWVQLTDERFGLEDPEDDICKYDFVEEPPSDGTL 120
 QY 121 GRWGSSTVPGKOISKNQIRIRFVSDYFPPSEPGFCIHNTVMPOTFEAVSPSVLPSPA 180
 DB 121 GRWGSSTVPGKOISKNQIRIRFVSDYFPPSEPGFCIHNTVMPOTFEAVSPSVLPSPA 180
 QY 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLDELYRPTWQLGKAFVGRKSRVVDLNL 240
 DB 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLDELYRPTWQLGKAFVGRKSRVVDLNL 240
 QY 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
 DB 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
 QY 301 VTKKHEVQLRPTKGVRLGKSLTDVALHHEBECDCVCRGSGTG 345
 DB 301 VTKKHEVQLRPTKGVRLGKSLTDVALHHEBECDCVCRGSGTG 345

RESULT 7
 AAB19578
 ID AAB19578 standard; protein; 345 AA.
 AC AAB19578;
 XX
 DT 22-JAN-2001 (first entry)
 DE Human PRO200 (vascular endothelial growth factor E).
 XX
 KW PRO200; vascular epithelial growth factor E; VEGF-E; human;
 KW ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa;
 KW macular degeneration; retinal detachment; retinal tear; macular hole;
 KW myopia; traumatic choriorretinopathy; acute retinal necrosis syndrome;
 KW contusion; edema; retinal vision occlusion; vascular disease;
 KW retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..14
 FT /label= Signal_peptide
 FT Protein 15..345
 FT /label= Mature_Pro200
 FT Modified-site 15..21
 FT /note= "N-myristoylation"
 FT Modified-site 25..29
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 55..59
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 117..123
 FT /note= "N-myristoylation"
 FT Modified-site 127..133
 FT /note= "N-myristoylation"
 FT Modified-site 254..258
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 281..287
 FT /note= "N-myristoylation"
 FT Modified-site 282..288
 FT /note= "N-myristoylation"
 FT Modified-site 319..325
 FT /note= "Amidation"
 XX
 PN MO20053760-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000MO-US006319.

XX 12-MAR-1999; 99US-0123957P.
 XX
 XX (GENTECH) INC.
 XX
 XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ,
 XX Kabakoff RC, Klein RD, Kljavin ID, Kuo SS, La Fleur M, Wood WI;
 XX WPI; 2000-587437/55.
 DR N-PSDB; AAA88515.
 XX
 PT Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.
 XX
 PS Claim 2; Fig 2; 140pp; English.
 CC
 CC The present sequence is that of human PRO200 or vascular endothelial
 CC growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515)
 CC that was isolated from a glioma cell line G61 library using probes (see
 CC AAA88523-26) based on an expressed sequence tag (see AAA88522) that
 CC showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a
 CC pI of about 6.06. A method for producing PRO polypeptides, including
 CC PRO200, using a host cell transformed with a vector comprising a PRO
 CC nucleic acid is claimed. The invention relates to the use of PRO
 CC polypeptides to delay, prevent or rescue retinal cells such as retinal
 CC neurons selected from photoreceptors, retinal ganglion cells, displaced
 CC retinal ganglion cells, amacrine cells, displaced amacrine cells,
 CC horizontal and bipolar neurons, and supportive cells (including Mueller
 CC cells and pigment epithelial cells) from injury and degeneration. The
 CC retinal cells are preferably photoreceptors and photoreceptor cell injury
 CC or death is caused by retinal injury, light or environmental trauma or by
 CC an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal tears,
 CC retinopathy, retinal degenerative diseases, macular holes, degenerative
 CC myopia, acute retinal necrosis syndrome, traumatic choriorretinopathies or
 CC contusion such as Purtscher's retinopathy, edema, ischemic conditions
 CC such as central or branch retinal vision occlusion, collagen vascular
 CC diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and
 CC occlusion associated with Fales disease and systemic lupus erythematosus
 CC (claimed)
 CC
 XX
 SQ Sequence 345 AA;
 Query Match 99.6%; Score 1851; DB 3; Length 345;
 Best Local Similarity 99.4%; Pred. No. 2, 2e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60
 DB 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60
 QY 61 PREPHYPRNTVYVWRLVAVEENWVQLTDERFGLEDPEDDICKYDFVEEPPSDGTL 120
 DB 61 PREPHYPRNTVYVWRLVAVEENWVQLTDERFGLEDPEDDICKYDFVEEPPSDGTL 120
 QY 121 GRWGSSTVPGKOISKNQIRIRFVSDYFPPSEPGFCIHNTVMPOTFEAVSPSVLPSPA 180
 DB 121 GRWGSSTVPGKOISKNQIRIRFVSDYFPPSEPGFCIHNTVMPOTFEAVSPSVLPSPA 180
 QY 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLDELYRPTWQLGKAFVGRKSRVVDLNL 240
 DB 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLDELYRPTWQLGKAFVGRKSRVVDLNL 240
 QY 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
 DB 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
 QY 301 VTKKHEVQLRPTKGVRLGKSLTDVALHHEBECDCVCRGSGTG 345
 DB 301 VTKKHEVQLRPTKGVRLGKSLTDVALHHEBECDCVCRGSGTG 345

RESULT 8

AA10651 ID AA10651 standard; protein, 345 AA.

XX AC AA10651;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X protein #3.

XX KM VEGF-X; vascular endothelial growth factor; human; vulnery; cytostratic; anti-rheumatic; anti-arthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burn; skin graft growth.

XX OS Homo sapiens.

XX PN MO20037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US030503.

XX PR 22-DEC-1998; 9AGB-00028377.

XX PR 18-MAR-1999; 99US-0124967P.

XX PR 08-NOV-1999; 99US-0164131P.

XX PA (JANNC) JANSSEN PHARM NV.

XX PI Gordon RD, Sprengel J, Von JR, Dijkman JH, Gosiowska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX PT New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds.

XX PT Claim 72; Fig 12; 127P; English.

XX PS This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnery, cytostratic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein described in the method of the invention

XX S0 Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 2.e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0

0Y 1 MSFGILLVTSALAGRGCTQAEISNLKSFQSSNKGQVODPQHERITVSTNGSIHS 60

Db 1 MSFGILLVTSALAGRGCTQAEISNLKSFQSSNKGQVODPQHERITVSTNGSIHS 60

0Y 61 PRPHTPTPNTLVWRLVAVEENWVQLTFDERFGLEDEDDICRKYDFVEEPPSGTLL 120

Db 61 PRPHTPTPNTLVWRLVAVEENWVQLTFDERFGLEDEDDICRKYDFVEEPPSGTLL 120

QY	121	GRWGSGGVPPCKQIISKNGQIRIRFVSDSEYPPSEBPCCHNYIVMPQFPAVSPSLPPSA	180
Db	121	GRWGSGGVPPCKQIISKNGQIRIRFVSDSEYPPSEBPCCHNYIVMPQFPAVSPSLPPSA	180
QY	181	LPDLIDNNALIAVAFSTLEDLIIVYLEEERQQLDLEDLYRFTWQLGKAFPGKRSRVVDNL	240
Db	181	LPDLIDNNALIAVAFSTLEDLIIVYLEEERQQLDLEDLYRFTWQLGKAFPGKRSRVVDNL	240
QY	241	LTEEVRLVSCTPRPNFSVSIREEIKRTDTITFMPCGLVYRCGNCACCLHNCBCCVPSK	300
Db	241	LTEEVRLVSCTPRPNFSVSIREEIKRTDTITFMPCGLVYRCGNCACCLHNCBCCVPSK	300
QY	301	VTKKYHEVLTQLRPKTVGRGLHKSLTDVALLEHNEBCDCVCRSGTGG	345
Db	301	VTKKYHEVLTQLRPKTVGRGLHKSLTDVALLEHNEBCDCVCRSGTGG	345
RESULT 9			
AAB10633			
ID	AAB10633 standard; protein, 345 AA.		
AC	AAB10633;		
XX			
DT	19-JAN-2001 (first entry)		
XX			
DE	Human RACE generated VEGF-X protein.		
XX			
VEGF-X;	vascular endothelial growth factor; human; vulnerable; cytostatic;		
KW	anti-rheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;		
KW	angiogenesis regulator; vascularization regulator; cancer; psoriasis;		
KW	rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;		
KW	tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;		
XX	venous sore; diabetic ulcer; burns; skin graft growth.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200037641-A2.		
PD	29-JUN-2000.		
XX			
PF	21-DEC-1999; 99WO-US030503.		
XX			
PR	22-DEC-1998; 98GB-00028377.		
PR	18-MAR-1999; 99US-0124967P.		
PR	08-NOV-1999; 99US-0164131P.		
XX			
PA	(JUNC) JANSSEN PHARM NV.		
XX			
PI	Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;		
PI	Dhanaraj SN, Xu J;		
XX			
DR	MPI; 2000-442669/38.		
XX	N-PSDB; AAA71951.		
XX			
PT	New vascular endothelial growth factor protein, useful for treating or		
PT	preventing diseases associated with inappropriate angiogenesis activity		
PT	such as cancer, rheumatoid arthritis, psoriasis and wounds.		
XX			
PS	Disclosure; Fig 6; 127pp; English.		
XX			
CC	This invention describes a novel vascular endothelial growth factor-X		
CC	(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has		
CC	vulnerery, cytostatic, anti-rheumatic, antiarthritic, antipsoriatic and		
CC	antidiabetic activity and acts as an angiogenesis and vascularization		
CC	regulator. An antisense molecule of the invention is useful for treating		
CC	or preventing cancer, rheumatoid arthritis, psoriasis and diabetic		
CC	retinopathy by inhibiting angiogenic activity or inappropriate		
CC	vascularization by inhibiting formation and proliferation of new blood		
CC	vessels, growth and development of tissues, tissue regeneration and organ		
CC	and tissue repair in a subject. The products of the invention are useful		
CC	for preparing medicaments for treating wounds such as dermal ulcers,		
CC	pressure sores, venous sores, diabetic ulcers and burns and to promote		
CC	skin graft growth, tissue repair, proliferation of new blood vessels,		

CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention

SO Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 2.2e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLFGLLTSALAGRGQAGQASNSLSKQFSSNKEQNGVDPQHERITITVSTNGSIHS 60
DB 1 MSLLFGLLTSALAGRGQAGQASNSLSKQFSSNKEQNGVDPQHERITITVSTNGSIHS 60
QY 61 PRPHPTYPRTVTLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
DB 61 PRPHPTYPRTVTLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQKISKGNQIRIRFVSDYFPPSEPGFCIHNYIWPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKQKISKGNQIRIRFVSDYFPPSEPGFCIHNYIWPQFTEAVSPSVLPSPA 180
QY 181 LPDLNLNNAITAFSTEDLIRYLEPERWQDLDELRYPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLNLNNAITAFSTEDLIRYLEPERWQDLDELRYPTWQLGKAFVGRKSRVVDNL 240
QY 241 LEEEVRLVSGTTPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCQVPSK 300
DB 241 LEEEVRLVSGTTPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCQVPSK 300
QY 301 VTKKHEVTLQLRPKTGVRGLHKSITDVALHHEBCDCVCRGSGTG 345
DB 301 VTKKHEVTLQLRPKTGVRGLHKSITDVALHHEBCDCVCRGSGTG 345

RESULT 10

AAB10650
ID AAB10650 standard; protein; 345 AA.

XX AAB10650;

DT 19-JUN-2001 (first entry)

XX Human 990126vegX protein.

DE VEGF-X; vascular endothelial growth factor; human; vulnery; cyrostatic;

KW antihumetic; antiarthritic; antiporiatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

OS WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US030503.

XX 22-DEC-1998; 98GB-00028377.

XX 18-MAR-1999; 99US-0124967P.

XX 08-NOV-1999; 99US-0164131P.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;
XX Dhanraj SN, Xu J;
XX WPI; 2000-442669/38.
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX Disclosure; Fig 11; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (1a) and its encoding polynucleotide (1a) which has
CC vulnery, cyrostatic, antihumetic, antiarthritic, antiporiatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation of tissues, tissue regeneration and organ
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human 990126vegX protein
CC used to illustrate the method of the invention

SO Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 2.2e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLFGLLTSALAGRGQAGQASNSLSKQFSSNKEQNGVDPQHERITITVSTNGSIHS 60
DB 1 MSLLFGLLTSALAGRGQAGQASNSLSKQFSSNKEQNGVDPQHERITITVSTNGSIHS 60
QY 61 PRPHPTYPRTVTLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
DB 61 PRPHPTYPRTVTLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQKISKGNQIRIRFVSDYFPPSEPGFCIHNYIWPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKQKISKGNQIRIRFVSDYFPPSEPGFCIHNYIWPQFTEAVSPSVLPSPA 180
QY 181 LPDLNLNNAITAFSTEDLIRYLEPERWQDLDELRYPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLNLNNAITAFSTEDLIRYLEPERWQDLDELRYPTWQLGKAFVGRKSRVVDNL 240
QY 241 LEEEVRLVSGTTPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCQVPSK 300
DB 241 LEEEVRLVSGTTPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCQVPSK 300
QY 301 VTKKHEVTLQLRPKTGVRGLHKSITDVALHHEBCDCVCRGSGTG 345
DB 301 VTKKHEVTLQLRPKTGVRGLHKSITDVALHHEBCDCVCRGSGTG 345

RESULT 11

AAB10635
ID AAB10635 standard; protein; 345 AA.

XX AAB10635;

DT 19-JUN-2001 (first entry)

XX Human VEGF-X protein #1 isolated from clones 4 and 7.

DE VEGF-X; vascular endothelial growth factor; human; vulnery; cyrostatic;

KW antihumetic; antiarthritic; antiporiatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

XX venous sore; diabetic ulcer; burns; skin graft growth.
XX Homo sapiens.
XX WO200037641-A2.

PD 29-JUN-2000.
 XX 21-DEC-1999; 99WO-US030503.
 XX 22-DEC-1998; 98GB-00028377.
 XX 18-MAR-1999; 99US-0124967P.
 XX 08-NOV-1999; 99US-0164131P.
 PA (JANC) JANSSEN PHARM NV.
 PI Gordon RD, Sprengel JI, Yon JR, Dijkmans JH, Gosiowska A;
 PI Dhanaraj SN, Xu J;
 XX WPI: 2000-442669/38.
 DR N-PSDB: AAA71955.
 XX
 PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
 XX
 PS Disclosure; Fig 9; 127pp; English.
 XX
 CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnerability, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the human VEGF-X protein
 CC isolated from clones 4 and 7 described in the method of the invention
 XX
 SQ Sequence 345 AA;
 Query Match 99.6%; Score 1851; DB 3; Length 345;
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVODPOHERIITVSTNGSIHS 60
 DB 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVODPOHERIITVSTNGSIHS 60
 QY 61 PRPHITPRNTVWLRVLAEBENWIOITDERFGLDEPDICIKYDFVEEESDGTIL 120
 DB 61 PRPHITPRNTVWLRVLAEBENWIOITDERFGLDEPDICIKYDFVEEESDGTIL 120
 QY 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFSPSEPGFCHNINIVMPQTEAVSPVLPPSA 180
 DB 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFSPSEPGFCHNINIVMPQTEAVSPVLPPSA 180
 QY 181 LPDLNNATITAFSTLEDLIRYLBEPWQDLLEDLYRPTWQLGKAFVFGKSRVVDLNT 240
 DB 181 LPDLNNATITAFSTLEDLIRYLBEPWQDLLEDLYRPTWQLGKAFVFGKSRVVDLNT 240
 QY 241 LTBREVRLVSCTPRPFNSVIRBELKRTDTIFWPGCLIVRCGNCACCLANECOCVPSK 300
 DB 241 LTBREVRLVSCTPRPFNSVIRBELKRTDTIFWPGCLIVRCGNCACCLANECOCVPSK 300
 QY 301 VTKKYHEVLQLRPKTGVGRLAKSLTDVALHEHBECDCCVCRSGTSG 345
 DB 301 VTKKYHEVLQLRPKTGVGRLAKSLTDVALHEHBECDCCVCRSGTSG 345

RESULT 12
 AAB10644
 ID AAB10644 standard; protein; 345 AA.

XX AAB10644;
 AC 19-JAN-2001 (first entry)
 DT Human VEGF-X protein #4.
 DE VEGF-X; vascular endothelial growth factor; human; vulnerable; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.
 XX
 OS Homo sapiens.
 XX
 XX WO200037641-A2.
 XX 29-JUN-2000.
 XX
 XX 21-DEC-1999; 99WO-US030503.
 XX
 XX 22-DEC-1998; 98GB-00028377.
 XX 18-MAR-1999; 99US-0124967P.
 XX 08-NOV-1999; 99US-0164131P.
 XX
 PA (JANC) JANSSEN PHARM NV.
 PI Gordon RD, Sprengel JI, Yon JR, Dijkmans JH, Gosiowska A;
 PI Dhanaraj SN, Xu J;
 XX WPI: 2000-442669/38.
 DR N-PSDB: AAA71950.
 XX
 PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
 XX
 PS Disclosure; Fig 30B; 127pp; English.
 XX
 CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnerability, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents a human VEGF-X protein
 CC described in the method of the invention
 XX
 SQ Sequence 345 AA;
 Query Match 99.6%; Score 1851; DB 3; Length 345;
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVODPOHERIITVSTNGSIHS 60
 DB 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVODPOHERIITVSTNGSIHS 60
 QY 61 PRPHITPRNTVWLRVLAEBENWIOITDERFGLDEPDICIKYDFVEEESDGTIL 120
 DB 61 PRPHITPRNTVWLRVLAEBENWIOITDERFGLDEPDICIKYDFVEEESDGTIL 120
 QY 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFSPSEPGFCHNINIVMPQTEAVSPVLPPSA 180
 DB 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFSPSEPGFCHNINIVMPQTEAVSPVLPPSA 180

Db 121 GRWCGSGTVPGKQISKGNQIRFVSDYPSSEPGFCIHNIIVMPQFTEAVSPSVLPSSA 180
 Qy 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240
 Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240
 Qy 241 LITEVRLYSCTPRNFSVSIRELKRITDTTFMPGCLLYKRCGACCLHNCNECCVPSK 300
 Db 241 LITEVRLYSCTPRNFSVSIRELKRITDTTFMPGCLLYKRCGACCLHNCNECCVPSK 300
 Qy 301 VTKKHYEVLQLRPKTGVRLGKSLTDVALHHEECDCVCGSTGG 345
 Db 301 VTKKHYEVLQLRPKTGVRLGKSLTDVALHHEECDCVCGSTGG 345

RESULT 13
 AAB44322
 ID AAB44322 standard; protein; 345 AA.
 AC AAB44322;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
 XX
 KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KM expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004341.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 29-MAR-1999; 99US-0126773P.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US028565.
 PR 30-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GENET) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filyaroff E, Fong S, Gao W, Gelber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI: 2000-611443/58.
 DR N-PDB: AAC78582.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.
 PS Claim 12; Fig 207; 636DP; English.
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence

CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytosolic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 XX
 SQ Sequence 345 AA:
 Qy 1 MSFLGILVTSALAGRRGTQAESNLSSKQPSNNKQNGVDPQDHRITTVSTNGSIHS 60
 Db 1 MSFLGILVTSALAGRRGTQAESNLSSKQPSNNKQNGVDPQDHRITTVSTNGSIHS 60
 Qy 61 PRPHTYPRNTVAVMLVAEENVMQLTFDERFGLDEPDDICXDPFVVEEPPDGTIL 120
 Db 61 PRPHTYPRNTVAVMLVAEENVMQLTFDERFGLDEPDDICXDPFVVEEPPDGTIL 120
 Qy 121 GRWCGSGTVPGKQISKGNQIRFVSDYPSSEPGFCIHNIIVMPQFTEAVSPSVLPSSA 180
 Db 121 GRWCGSGTVPGKQISKGNQIRFVSDYPSSEPGFCIHNIIVMPQFTEAVSPSVLPSSA 180
 Qy 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240
 Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240
 Qy 241 LITEVRLYSCTPRNFSVSIRELKRITDTTFMPGCLLYKRCGACCLHNCNECCVPSK 300
 Db 241 LITEVRLYSCTPRNFSVSIRELKRITDTTFMPGCLLYKRCGACCLHNCNECCVPSK 300
 Qy 301 VTKKHYEVLQLRPKTGVRLGKSLTDVALHHEECDCVCGSTGG 345
 Db 301 VTKKHYEVLQLRPKTGVRLGKSLTDVALHHEECDCVCGSTGG 345

RESULT 14
 AAB24412
 ID AAB24412 standard; protein; 345 AA.
 AC AAB24412;
 XX
 DT 07-NOV-2000 (first entry)
 DE Human PRO713 protein sequence SEQ ID NO:137.
 XX
 KM Human; PRO; promotion; inhibition; angiogenesis; cardiovascularization;
 KM diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KM angiogenic; proliferative; cardiac; cardiovascular; antihtherosclerotic;
 KM cytosolic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200032221-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US028313.
 XX
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 12-JAN-1999; 99US-0115554P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.

```

PR      23 -JUN-1999;    99US-0141037P.
PR      20 -JUN-1999;    99US-0144758P.
PR      26 -JUL-1999;    99US-0146598P.
PR      01 -SEP-1999;    99WO-US020111.
PR      08 -SEP-1999;    99WO-US020594.
PR      13 -SEP-1999;    99WO-US020944.
PR      15 -SEP-1999;    99WO-US021090.
PR      15 -SEP-1999;    99WO-US021547.
PR      05 -OCT-1999;    99WO-US023089.
PR      29 -OCT-1999;    99US-0162506P.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ,
XX      Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF,
XX      Smith V, Watanabe CK, Williams PM, Wood WI,
XX      MPI: 2000-412154/35.
XX      N-PSDB; AAA77621.
XX
XX      Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
XX      PT and treating diagnosing a cardiovascular, endothelial or angiogenic
XX      disorders in mammals.
XX
XX      Claim 72; Fig 50; 315pp; English.
XX
XX      The present invention describes nucleic acids encoding PRO polypeptides
XX      CC useful for preventing, diagnosing and treating diagnosing a
XX      CC cardiovascular, endothelial or angiogenic disorder in mammals by
XX      CC modulating cell proliferation, angiogenesis and cardiovascularisation,
XX      CC and for identifying agonists and antagonists of these processes. The
XX      CC nucleic acids and the proteins they encode may be used in the prevention,
XX      CC treatment and diagnosis of diseases associated with inappropriate PRO
XX      CC expression such as cardiovascular, endothelial or angiogenic disorders in
XX      CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
XX      CC example, the nucleic acids (Ncs) and vectors containing them and the PRO
XX      CC polypeptide may be used to treat disorders associated with decreased PRO
XX      CC expression. AAA77510 to AAA77721 and AAB2438 to AAB24435 represent
XX      CC nucleotide and protein sequences used in the exemplification of the
XX      CC present invention
XX
XX      Sequence 345 AA;
XX
XX      Query Match          99.6%; Score 1851; DB 3; Length 345;
XX      Best Local Similarity 99.4%; Pred. No. 2, 2e-178;
XX      Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0
XX
QY      1 MSLRGLLVTSALAGORNGTQAESLUSKFGQSSNKEONGVODPOHERITVSTNGSIHS 60
DB      1 MSLRGLLVTSALAGORNGTQAESLUSKFGQSSNKEONGVODPOHERITVSTNGSIHS 60
QY      61 PRPPTTYRNTVYLWRLVAVEENVYIOLTPDERFGLDEPEDDICKYDFAVEVSPSDGTL 120
DB      61 PRPPTTYRNTVYLWRLVAVEENVYIOLTPDERFGLDEPEDDICKYDFAVEVSPSDGTL 120
QY      121 GRWGSGTVPGKQISKNGQIRIRFVSDSEVFPSPFCIHYNIVMPQFTEAVSPSYLPSBA 180
DB      121 GRWGSGTVPGKQISKNGQIRIRFVSDSEVFPSPFCIHYNIVMPQFTEAVSPSYLPSBA 180
QY      121 GRWGSGTVPGKQISKNGQIRIRFVSDSEVFPSPFCIHYNIVMPQFTEAVSPSYLPSBA 180
DB      121 GRWGSGTVPGKQISKNGQIRIRFVSDSEVFPSPFCIHYNIVMPQFTEAVSPSYLPSBA 180
QY      181 LPDLILNNAITAFSTLEDLIRYLEPERNOLEDLIDYRPTWQLGKAFVFGKRSRVVDLNL 240
DB      181 LPDLILNNAITAFSTLEDLIRYLEPERNOLEDLIDYRPTWQLGKAFVFGKRSRVVDLNL 240
QY      241 LTBEEVRLVSCPRNPSVSIIRBELKKTDTITFMWGCLLYVRGCGNACCLHNCECCQVBSK 300
DB      241 LTBEEVRLVSCPRNPSVSIIRBELKKTDTITFMWGCLLYVRGCGNACCLHNCECCQVBSK 300
QY      301 VTKKYHEVTLQLRPKTVGRLGKSLTDVALLEHHEECDCVCRGSGTG 345
DB      301 VTKKYHEVTLQLRPKTVGRLGKSLTDVALLEHHEECDCVCRGSGTG 345

```

AAVS9285	AAVS9285 standard; protein; 345 AA.
ID	AAVS9285 standard; protein; 345 AA.
AC	AAVS9285;
XX	
XX	
DT	25-APR-2000 (first entry)
XX	
DE	Bone morphogenic protein (BMP) (clone HETAB62).
XX	
KW	Bone morphogenic protein; BMP; cytosolic; osteopathic; angiogenic;
KW	vulnerary; bone disorder; osteoarthritis; cartilage defect; human;
XX	tissue repair; gene therapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	1..22
FT	/note= "signal peptide"
FT	15..26
FT	/note= "immunogenic epitope"
FT	23..345
FT	/note= "mature protein"
FT	33..46
FT	/note= "immunogenic epitope"
FT	133..138
FT	/note= "immunogenic epitope"
FT	214..220
FT	/note= "immunogenic epitope"
FT	249..255
FT	/note= "immunogenic epitope"
FT	261..267
FT	/note= "immunogenic epitope"
XX	
PN	WO200004183-A1.
XX	
PD	27-JAN-2000.
XX	
PF	14-JUL-1999; 99WO-US015783.
XX	
PR	15-JUL-1998; 98US-0092922P.
XX	
PA	(HUMA-) HUMAN GENOME SCT INC.
XX	
PI	Ruben SM, Young PE;
XX	
DR	MP1: 2000-182442/16.
XX	N-P8DB; AAZ48599.
XX	
PT	Novel cDNA encoding human bone morphogenic proteins, vectors, host cells
PT	and methods of recombinant production, useful for diagnosis and treatment
XX	of, e.g. bone disorders.
XX	
P3	Claim 11; Page 183-184; 187pp; English.
XX	
CC	The invention provides novel human bone morphogenic proteins (BMP) and
CC	nucleic acids encoding the BMPs. The BMP polypeptides can be expressed by
CC	standard recombinant methodology. Determining the presence or absence of
CC	a mutation in the polynucleotides or determining the presence or amount
CC	of expression in the polynucleotides is useful for diagnosing a pathological
CC	condition or a susceptibility to a pathological condition in a subject.
CC	The polynucleotides can also be used to prevent, treat or ameliorate a
CC	medical condition. The proteins are useful for diagnosis and/or treatment
CC	of diseases associated with BMPs, in particular bone disorders (e.g.
CC	osteoarthritis, cartilage defects and tissue repair), and in particular
CC	for stimulation of angiogenesis. The polynucleotides are useful as
CC	reagents for differential identification of tissues or cell types present
CC	in biological samples. The polynucleotides can be used in gene therapy to
CC	promote the growth of endothelial cells. The present sequence represents
XX	a BMP of the invention (clone HETAB62)
XX	
SQ	Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 2.2e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKKEONGVODPOHERITTSNGSIHS 60
Db      1  MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKKEONGVODPOHERITTSNGSIHS 60
QY      61  PRPFHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPEDDICKYDFVEVEEESDGTIL 120
Db      61  PRPFHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPEDDICKYDFVEVEEESDGTIL 120
QY     121  GRMCGSGTVPGKOISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPSLPPSA 180
Db     121  GRMCGSGTVPGKOISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPSLPPSA 180
QY     181  LPDLNNATTAFTLEDLIRYLEPERMQLDEDLRPTWQLGKAFVFGKRSRVVDNL 240
Db     181  LPDLNNATTAFTLEDLIRYLEPERMQLDEDLRPTWQLGKAFVFGKRSRVVDNL 240
QY     241  LTEEVRLYSCTPRNFVSYSIREBELKRTDTIFWPGCLVKGCGNCAACCIANCNBQCVPSPK 300
Db     241  LTEEVRLYSCTPRNFVSYSIREBELKRTDTIFWPGCLVKGCGNCAACCIANCNBQCVPSPK 300
QY     301  VTKKYHEVLDQRPKTVGRGLHKSITDVALSHHEECDCVCRGSTGG 345
Db     301  VTKKYHEVLDQRPKTVGRGLHKSITDVALSHHEECDCVCRGSTGG 345

```

Search completed: May 27, 2004, 15:44:44
Job time : 54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:42:51 ; Search time 16.5 Seconds
(without alignments)
1079.452 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1858
Sequence: 1 MSFLGLLVTLSALAGORRGT.....DVALEHHEBCDVCGRSGTG 345

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appli
2	1851	99.6	345	US-09-457-066-2	Sequence 2, Appli
3	1851	99.6	345	US-09-265-686-2	Sequence 2, Appli
4	1851	99.6	345	US-09-540-224-5	Sequence 5, Appli
5	1851	99.6	345	US-09-564-595D-33	Sequence 33, Appli
6	1851	99.6	345	US-09-706-968-2	Sequence 2, Appli
7	1851	99.6	345	US-09-723-749-2	Sequence 2, Appli
8	1851	99.6	345	US-09-823-033-2	Sequence 2, Appli
9	1664	89.6	345	US-09-457-066-43	Sequence 43, Appli
10	1664	89.6	345	US-09-564-595D-35	Sequence 35, Appli
11	1664	89.6	345	US-09-706-968-43	Sequence 43, Appli
12	1664	89.6	345	US-09-823-033-4	Sequence 54, Appli
13	1325	71.3	302	US-09-564-595D-54	Sequence 54, Appli
14	1266.5	68.2	303	US-09-564-595D-57	Sequence 57, Appli
15	1098	59.1	316	US-09-564-595D-55	Sequence 55, Appli
16	1051.5	56.6	317	US-09-564-595D-56	Sequence 56, Appli
17	741.5	39.9	370	US-09-457-066-37	Sequence 37, Appli
18	741.5	39.9	370	US-09-540-224-2	Sequence 2, Appli
19	741.5	39.9	370	US-09-564-595D-2	Sequence 2, Appli
20	741.5	39.9	370	US-09-706-968-37	Sequence 37, Appli
21	741.5	39.9	370	US-09-808-972-2	Sequence 2, Appli
22	741.5	39.9	370	US-09-823-033-5	Sequence 5, Appli
23	737.5	39.7	370	US-09-540-224-4	Sequence 4, Appli
24	737.5	39.7	370	US-09-564-595D-53	Sequence 53, Appli
25	737.5	39.7	370	US-09-808-972-4	Sequence 4, Appli
26	180	9.7	53	US-09-621-976-5212	Sequence 5212, Ap
27	173	9.3	3623	US-09-341-461-2	Sequence 2, Appli

28	172.5	9.3	730	3	US-08-872-757-2	Sequence 2, Appli
29	172.5	9.3	730	4	US-09-850-048A-2	Sequence 2, Appli
30	172	9.3	1012	4	US-09-285-385C-4	Sequence 4, Appli
31	171	9.2	1015	4	US-09-285-385C-2	Sequence 2, Appli
32	169	9.1	788	1	US-08-572-225-1	Sequence 1, Appli
33	169	9.1	986	4	US-09-285-385C-19	Sequence 19, Appli
34	164.5	8.9	909	3	US-08-936-135-18	Sequence 18, Appli
35	164.5	8.9	909	4	US-09-439-711C-18	Sequence 18, Appli
36	164.5	8.9	926	3	US-08-936-135-20	Sequence 20, Appli
37	164.5	8.9	926	4	US-09-439-711C-20	Sequence 20, Appli
38	164.5	8.9	931	4	US-09-583-638-4	Sequence 4, Appli
39	163.5	8.8	921	4	US-09-439-711C-4	Sequence 4, Appli
40	163.5	8.8	922	4	US-09-116-473-4	Sequence 4, Appli
41	163	8.8	101	3	US-09-374-135-6	Sequence 6, Appli
42	160.5	8.6	925	4	US-09-116-473-2	Sequence 2, Appli
43	160.5	8.6	901	3	US-08-936-135-22	Sequence 22, Appli
44	160.5	8.6	901	4	US-09-439-711C-22	Sequence 22, Appli
45	160.5	8.6	906	3	US-08-936-135-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-09-040-220D-2
; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match	99.6%	Score 1851;	DB 4;	Length 345;
Beet Local Similarity	99.4%	Pred. No. 6.2e-193;		
Matches 343;	Conservative	2;	Mismatches 0;	Indels 0;
Gaps 0;				
Qy	1	MSFLGLLVTLSALAGORRGTQAESNLSKSFQFSNKEONGVQDPQHERITVSTNGSIHS	60	
Db	1	MSFLGLLVTLSALAGORRGTQAESNLSKSFQFSNKEONGVQDPQHERITVSTNGSIHS	60	
Qy	61	PRFPHYPRNTVLVWLRVAEENWVQLTDERGLEDPEBDICXYDFVEVEPSDGTIL	120	
Db	61	PRFPHYPRNTVLVWLRVAEENWVQLTDERGLEDPEBDICXYDFVEVEPSDGTIL	120	
Qy	121	GRWCGSGTVGKQISKNOIRIRFVSDEYPPSEGFICHTNINWQTEAVSPVLPPSA	180	
Db	121	GRWCGSGTVGKQISKNOIRIRFVSDEYPPSEGFICHTNINWQTEAVSPVLPPSA	180	
Qy	121	GRWCGSGTVGKQISKNOIRIRFVSDEYPPSEGFICHTNINWQTEAVSPVLPPSA	180	
Db	121	GRWCGSGTVGKQISKNOIRIRFVSDEYPPSEGFICHTNINWQTEAVSPVLPPSA	180	
Qy	181	LPDLNNATITAFSTEDLIRYLEPERWQDLEDPYPTWOLGKAVFGKRSVVDNL	240	
Db	181	LPDLNNATITAFSTEDLIRYLEPERWQDLEDPYPTWOLGKAVFGKRSVVDNL	240	
Qy	241	LTEEVRRLYSCPRNFVSIREELKRTDTIFWPGCLVRCGNCACCIHNCNECQVPSK	300	
Db	241	LTEEVRRLYSCPRNFVSIREELKRTDTIFWPGCLVRCGNCACCIHNCNECQVPSK	300	
Qy	301	VTKKTHEVLDLRPKTGVRLGKSLTDVALHHEBCDVCGRSGTG	345	
Db	301	VTKKTHEVLDLRPKTGVRLGKSLTDVALHHEBCDVCGRSGTG	345	

RESULT 2
 US-09-457-066-2
 ; Sequence 2, Application US/09457066
 ; Patent No. 6432673
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Shoemaker, Kimberly E.
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: West, James W.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
 ; FILE REFERENCE: 98-60
 ; CURRENT APPLICATION NUMBER: US/09/457,066
 ; CURRENT FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-457-066-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
 Best Local Similarity 99.4%; Pred. No. 6.2e-193;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLTVTSALAGRGTOAESNLSSKFOSSNKEQGVDPQHERITVSTNGSIHS 60
 DB 1 MSFGLLTVTSALAGRGTOAESNLSSKFOSSNKEQGVDPQHERITVSTNGSIHS 60
 QY 61 PRPHYPRNTVLMWLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
 DB 61 PRPHYPRNTVLMWLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
 QY 121 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 DB 121 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 QY 122 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 DB 122 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 QY 181 LPDDLNNAITAFSTLEDLIRYLEPERMQLDLEDLIRPTWQLLGKAFVGRKSRVVDNL 240
 DB 181 LPDDLNNAITAFSTLEDLIRYLEPERMQLDLEDLIRPTWQLLGKAFVGRKSRVVDNL 240
 QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
 DB 241 LEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
 QY 301 VTKKHEVLQLRPKTGVRLGHSKLTDLVALEHHECCDVCGRSTGG 345
 DB 301 VTKKHEVLQLRPKTGVRLGHSKLTDLVALEHHECCDVCGRSTGG 345

RESULT 3
 US-09-265-686-2
 ; Sequence 2, Application US/09265686
 ; Patent No. 6455283
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Kuo, Sophia S.
 ; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
 ; FILE REFERENCE: P1122P2
 ; CURRENT APPLICATION NUMBER: US/09/265,686
 ; CURRENT FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: US 09/040,220
 ; PRIOR FILING DATE: 1998-03-17
 ; PRIOR APPLICATION NUMBER: US 09/184,216
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 8
 ; SEQ ID NO 2
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Human

US-09-265-686-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
 Best Local Similarity 99.4%; Pred. No. 6.2e-193;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLTVTSALAGRGTOAESNLSSKFOSSNKEQGVDPQHERITVSTNGSIHS 60
 DB 1 MSFGLLTVTSALAGRGTOAESNLSSKFOSSNKEQGVDPQHERITVSTNGSIHS 60
 QY 61 PRPHYPRNTVLMWLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
 DB 61 PRPHYPRNTVLMWLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
 QY 121 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 DB 121 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 QY 181 LPDDLNNAITAFSTLEDLIRYLEPERMQLDLEDLIRPTWQLLGKAFVGRKSRVVDNL 240
 DB 181 LPDDLNNAITAFSTLEDLIRYLEPERMQLDLEDLIRPTWQLLGKAFVGRKSRVVDNL 240
 QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
 DB 241 LEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
 QY 301 VTKKHEVLQLRPKTGVRLGHSKLTDLVALEHHECCDVCGRSTGG 345
 DB 301 VTKKHEVLQLRPKTGVRLGHSKLTDLVALEHHECCDVCGRSTGG 345

RESULT 4
 US-09-540-224-5
 ; Sequence 5, Application US/09540224
 ; Patent No. 6468343
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: Hart, Charles E.
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 ; FILE REFERENCE: 00-28
 ; CURRENT APPLICATION NUMBER: US/09/540,224
 ; EARLIER FILING DATE: 2000-03-31
 ; EARLIER APPLICATION NUMBER: US 60/180,169
 ; EARLIER FILING DATE: 2000-02-04
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-540-224-5

Query Match 99.6%; Score 1851; DB 4; Length 345;
 Best Local Similarity 99.4%; Pred. No. 6.2e-193;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLTVTSALAGRGTOAESNLSSKFOSSNKEQGVDPQHERITVSTNGSIHS 60
 DB 1 MSFGLLTVTSALAGRGTOAESNLSSKFOSSNKEQGVDPQHERITVSTNGSIHS 60
 QY 61 PRPHYPRNTVLMWLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
 DB 61 PRPHYPRNTVLMWLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
 QY 121 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 DB 121 GRWCGGTVPKGQISKNGQIRIRFVSDEYFSPGFCIHYNVMPQTEAVSPVLPSA 180
 QY 181 LPDDLNNAITAFSTLEDLIRYLEPERMQLDLEDLIRPTWQLLGKAFVGRKSRVVDNL 240
 DB 181 LPDDLNNAITAFSTLEDLIRYLEPERMQLDLEDLIRPTWQLLGKAFVGRKSRVVDNL 240

QY 241 LTBELVRLYSCPRNFVSIRBELKRTDTITFMPGCLLVRCGNCACCLHNCNCCQVPSK 300
DB 241 LTBELVRLYSCPRNFVSIRBELKRTDTITFMPGCLLVRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHEHECDVCVCRSGTG 345
DB 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHEHECDVCVCRSGTG 345

RESULT 5

US-09-564-595D-33
Sequence 33, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-595D-33

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 6.2e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAEENWVQLTDERFGLDEPDICKYDFVEVEEBSDGTIL 120
DB 61 PRPHTYPRNTVLVWRLVAEENWVQLTDERFGLDEPDICKYDFVEVEEBSDGTIL 120
QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPESEPGFCIHNIIVMPQTEAVSPSLPPSA 180
DB 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPESEPGFCIHNIIVMPQTEAVSPSLPPSA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAFVFGKRSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAFVFGKRSRVVDNL 240
QY 241 LTBELVRLYSCPRNFVSIRBELKRTDTITFMPGCLLVRCGNCACCLHNCNCCQVPSK 300
DB 241 LTBELVRLYSCPRNFVSIRBELKRTDTITFMPGCLLVRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHEHECDVCVCRSGTG 345
DB 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHEHECDVCVCRSGTG 345

RESULT 6

US-09-706-968-2
Sequence 2, Application US/09706968
Patent No. 6528050
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.

APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-706-968-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 6.2e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAEENWVQLTDERFGLDEPDICKYDFVEVEEBSDGTIL 120
DB 61 PRPHTYPRNTVLVWRLVAEENWVQLTDERFGLDEPDICKYDFVEVEEBSDGTIL 120
QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPESEPGFCIHNIIVMPQTEAVSPSLPPSA 180
DB 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPESEPGFCIHNIIVMPQTEAVSPSLPPSA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAFVFGKRSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAFVFGKRSRVVDNL 240
QY 241 LTBELVRLYSCPRNFVSIRBELKRTDTITFMPGCLLVRCGNCACCLHNCNCCQVPSK 300
DB 241 LTBELVRLYSCPRNFVSIRBELKRTDTITFMPGCLLVRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHEHECDVCVCRSGTG 345
DB 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHEHECDVCVCRSGTG 345

RESULT 7

US-09-723-749-2
Sequence 2, Application US/09723749
Patent No. 6620784
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
FILE REFERENCE: P1122P201
CURRENT APPLICATION NUMBER: US/09/723,749
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/265,666
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-723-749-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 6.2e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSIFGLLVTSLAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSIFGLLVTSLAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDIDCKYDFVEEPPSDGTL 120
DB 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDIDCKYDFVEEPPSDGTL 120
QY 121 GRWGSSTGPGKQISKNOIRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPSPA 180
DB 121 GRWGSSTGPGKQISKNOIRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPSPA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240
QY 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTITFPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTITFPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKHEVLOLRPKTGVGRLHKSITDVALHEHBECDVCRCGSTG 345
DB 301 VTKKHEVLOLRPKTGVGRLHKSITDVALHEHBECDVCRCGSTG 345

```

```

RESULT 8
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. 663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-823-033-2

```

```

Query Match          99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 6.2e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSIFGLLVTSLAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSIFGLLVTSLAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDIDCKYDFVEEPPSDGTL 120
DB 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDIDCKYDFVEEPPSDGTL 120
QY 121 GRWGSSTGPGKQISKNOIRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPSPA 180
DB 121 GRWGSSTGPGKQISKNOIRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPSPA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240
QY 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTITFPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTITFPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKHEVLOLRPKTGVGRLHKSITDVALHEHBECDVCRCGSTG 345
DB 301 VTKKHEVLOLRPKTGVGRLHKSITDVALHEHBECDVCRCGSTG 345

```

```

RESULT 9
US-09-457-066-43
; Sequence 43, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PR
; ORGANISM: Mus musculus
US-09-457-066-43

```

```

Query Match          89.6%; Score 1664; DB 4; Length 345;
Best Local Similarity 86.7%; Pred. No. 1.4e-172;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 1 MSIFGLLVTSLAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSIFGLLVTSLAGRGRTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDIDCKYDFVEEPPSDGTL 120
DB 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDIDCKYDFVEEPPSDGTL 120
QY 121 GRWGSSTGPGKQISKNOIRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPSPA 180
DB 121 GRWGSSTGPGKQISKNOIRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPSPA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240
QY 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTITFPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTITFPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKHEVLOLRPKTGVGRLHKSITDVALHEHBECDVCRCGNAGG 345
DB 301 VTKKHEVLOLRPKTGVGRLHKSITDVALHEHBECDVCRCGNAGG 345

```

```

RESULT 10
US-09-564-595D-35
; Sequence 35, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04

```

NUMBER OF SEQ ID NOS: 57
 SOFTWARE: PaetsEQ for Windows Version 4.0
 SEQ ID NO 35
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-564-595D-35

Query Match 89.6%; Score 1664; DB 4; Length 345;
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVTNGSIHS 60
 DB 1 MLGLGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVTNGSIHS 60
 QY 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
 DB 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
 QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDYFSEBPGFCIHNYIWPQTEAVSPSVLPSSA 180
 DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDYFSEBPGFCIHYSIIMPQVETTSPSVLPSS 180
 QY 181 LPDLNNATAPSTLEDLIRYLEPERWQDLDELYPTWQLGKAFVGRKSRVNDL 240
 DB 181 LSLDLNNATAPSTLEDLIRYLEPERWQDLDELYPTWQLGKAFVGRKSRVNDL 240
 QY 241 LTBVRLVYSCTPRNFVSIRBELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCQVPSK 300
 DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCQVPSK 300
 QY 301 VTKKYHEVLQLRPKTVGVLGKLSITDVALHHEBDCVCRCSTGG 345
 DB 301 VTKKYHEVLQLRPKTVGVLGKLSITDVALHHEBDCVCRCSTGG 345

RESULT 11
 US-09-706-968-43
 Sequence 43, Application US/09706968
 Patent No. 6528050
 GENERAL INFORMATION:
 APPLICANT: Gao, Zeren
 APPLICANT: Hart, Charles E.
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Shoemaker, Kimberly E.
 APPLICANT: Gilbertson, Debra G.
 TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFS
 FILE REFERENCE: 98-60C1
 CURRENT APPLICATION NUMBER: US/09/706, 968
 CURRENT FILING DATE: 2000-11-06
 PRIOR APPLICATION NUMBER: US/09/541, 752
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PaetsEQ for Windows Version 3.0
 SEQ ID NO 43
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-706-968-43

Query Match 89.6%; Score 1664; DB 4; Length 345;
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVTNGSIHS 60
 DB 1 MLGLGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVTNGSIHS 60
 QY 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
 DB 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120

DB 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGSVL 120
 QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDYFSEBPGFCIHNYIWPQTEAVSPSVLPSSA 180
 DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDYFSEBPGFCIHYSIIMPQVETTSPSVLPSS 180
 QY 181 LPDLNNATAPSTLEDLIRYLEPERWQDLDELYPTWQLGKAFVGRKSRVNDL 240
 DB 181 LSLDLNNATAPSTLEDLIRYLEPERWQDLDELYPTWQLGKAFVGRKSRVNDL 240
 QY 241 LTBVRLVYSCTPRNFVSIRBELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCQVPSK 300
 DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCQVPSK 300
 QY 301 VTKKYHEVLQLRPKTVGVLGKLSITDVALHHEBDCVCRCSTGG 345
 DB 301 VTKKYHEVLQLRPKTVGVLGKLSITDVALHHEBDCVCRCSTGG 345

RESULT 12
 US-09-823-033-4
 Sequence 4, Application US/09823033
 Patent No. 6663870
 GENERAL INFORMATION:
 APPLICANT: Hart, Charles E.
 APPLICANT: Gilbertson, Debra G.
 TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 FILE REFERENCE: 00-12
 CURRENT APPLICATION NUMBER: US/09/823, 033
 CURRENT FILING DATE: 2001-03-29
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PaetsEQ for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-823-033-4

Query Match 89.6%; Score 1664; DB 4; Length 345;
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVTNGSIHS 60
 DB 1 MLGLGLLVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVTNGSIHS 60
 QY 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
 DB 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120

```

; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

```

```

Query Match      71.3%; Score 1325; DB 4; Length 302;
Best Local Similarity 82.8%; Pred. No. 9.5e-136;
Matches 246; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

```

```

QY 46 HERIITVSTNGSIHSPRPHTYPRNTVLYWRLVAEENWVIOITPDERFGLDEPDEDICK 105
DB 1 HERIITVSTNGSIHSPRPHTYPRNTVLYWRLVAEENWVIOITPDERFGLDEPDEDICK 60
QY 106 YDFVEVEEPESDGTLIGRWCGSGTVPGKOISKNOQIRIFVSDSEYFSEPGFCIHNYIWP 165
DB 61 YDFVEVEEPESDGTLIGRWCGSGTVPGKOISKNOQIRIFVSDSEYFSEPGFCIHNYIWP 120
QY 166 QFTEAVSPSLPPSALPLDLNNATFSTLEDLIRLLEPERNOQDLEDLYRPTWOLGK 225
DB 121 QFTEAVSPSLPPSALPLDLNNATFSTLEDLIRLLEPERNOQDLEDLYRPTWOLGK 180
QY 226 AFVGRKSRVVDNLITTEEVRLYSCTPRNFSVIREELKRTDTIFMPGCLLVKRCGNGCA 285
DB 181 AFVGRKSRVVDNLITTEEVRLYSCTPRNFSVIREELKRTDTIFMPGCLLVKRCGNGCG 239
QY 286 CCLANECOCVPSKYTKYHEVLOLRP--KTGVGRHKSLTDVALHHEBCDCVYC 339
DB 240 CGVTVNRSCCTGNGSKYTKYHEVLOLRP--KTGVGRHKSLTDVALHHEBCDCVYC 296

```

```

RESULT 14
US-09-564-595D-57
; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

```

```

Query Match      68.2%; Score 1266.5; DB 4; Length 303;
Best Local Similarity 78.9%; Pred. No. 2.2e-129;
Matches 240; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

```

```

QY 47 ERITVSTNGSIHSPRPHTYPRNTVLYWRLVAEENWVIOITPDERFGLDEPDEDICK 106
DB 2 DETIQKNGGVYSPSPFNYSYRNLLITRLHS-QENTIQVFNQDQGLBEKENDICRY 60
QY 107 DFVEVEEPESDGT--IIGRWCGSGTVPGKOISKNOQIRIFVSDSEYFSEPGFCIHNYIWP 164
DB 61 DFVEVEEPESDGT--IIGRWCGSGTVPGKOISKNOQIRIFVSDSEYFSEPGFCIHNYIWP 119
QY 165 PQFTEA---VSPVLPSPALPLDLNNATFSTLEDLIRLLEPERNOQDLEDLYRPTW 221
DB 120 EDFQPAASVSPSALPLDLNNATFSTLEDLIRLLEPERNOQDLEDLYRPTW 179
QY 222 LIGKAFVGRKSRVVDNLITTEEVRLYSCTPRNFSVIREELKRTDTIFMPGCLLVKRCG 281
DB 180 LIGKAFVGRKSRVVDNLITTEEVRLYSCTPRNFSVIREELKRTDTIFMPGCLLVKRCG 239
QY 282 GNCACCLANECOCVPSKYTKYHEVLOLRPTGYRGHKSLTDVALHHEBCDCVYC 341
DB 240 GNCACCLANECOCVPSKYTKYHEVLOLRPTGYRGHKSLTDVALHHEBCDCVYC 299
QY 342 STGG 345
DB 300 STGG 303

```

```

RESULT 15
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

```

```

Query Match      59.1%; Score 1098; DB 4; Length 316;
Best Local Similarity 67.1%; Pred. No. 5.3e-111;
Matches 210; Conservative 26; Mismatches 55; Indels 22; Gaps 5;

```

```

QY 46 HERIITVSTNGSIHSPRPHTYPRNTVLYWRLVAEENWVIOITPDERFGLDEPDEDICK 105
DB 1 HERIITVSTNGSIHSPRPHTYPRNTVLYWRLVAEENWVIOITPDERFGLDEPDEDICK 60
QY 106 YDFVEVEEPESDGTLIGRWCGSGTVPGKOISKNOQIRIFVSDSEYFSEPGFCIHNYIWP 165
DB 61 YDFVEVEEPESDGTLIGRWCGSGTVPGKOISKNOQIRIFVSDSEYFSEPGFCIHNYIWP 120
QY 166 QFTEAV-----SPSVLPSPALPLDLNNATFSTLEDLIRLLEPERNO 209

```

```

Db      121  QPTEAETWSESVTSSISGVSYNPSVTDPT-LIADALDKXIAEFDVEDLKYFNPSWQ 179
QY      210  LDLEDLYRPTWQJGKAFVFGKSRVNDLILTEEVRLXCTPRNFSYSIREELKRTDTI 269
Db      180  EDLENMYLDTPRYGRGRY-HDKRSK-VDLRLINDAKRYSCTPRNVSYNIREELKLANV 237
QY      270  FMPGCLLVKRCGNCACCLHNCNECQCVPSKYTKKYEVLQLRP--KTGVRGLHKSLTD 326
Db      238  FFPRLVYQRCGNCGCTVWWRSTCNSGKTVKKYHEVLOPEFGHFKRGRAKTMALVD 297
QY      327  VALHHHEECDCVC 339
Db      298  IQLDHHERCDCIC 310

```

Search completed: May 27, 2004, 15:48:08
 Job time : 17.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:56 ; Search time 14 Seconds
(without alignments)
2370.434 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858
Sequence: 1 MSLEGLLVTSALAGQRGRGT.....DVALEHHBECDVCGRGTGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742.5	40.0	370	2	UC7591
2	737.5	39.7	370	2	UC7598
3	736	39.6	370	2	UC7592
4	183	9.8	3623	2	TC9456
5	181.5	9.8	730	1	BMH1
6	179.5	9.7	927	1	J00948
7	176	9.5	707	2	JC2218
8	176	9.5	3623	2	TC9456
9	173	9.3	823	1	AS8788
10	169	9.1	991	2	I49540
11	154	8.3	449	2	A55362
12	154	8.0	1057	1	A39288
13	148.5	7.7	686	1	A59271
14	143.5	7.5	1070	2	T31069
15	139.5	7.5	597	2	S71352
16	138.5	7.4	705	1	CIHURB
17	138	7.4	699	1	I54763
18	137.5	7.4	1524	2	T30337
19	137.5	7.3	533	2	UC7985
20	135	7.2	1594	2	T30549
21	133	7.1	419	2	S69207
22	130.5	7.0	1464	2	JS8984
23	128	6.9	402	2	JH0403
24	127.5	6.9	757	2	T30018
25	127.5	6.9	3871	2	T22812
26	125	6.7	198	2	JS0735
27	123.5	6.6	277	2	A41735
28	123.5	6.6	579	2	JC7629
29	123.5	6.6	579	2	JC7629

30	120.5	6.5	245	1	TWCSS	platelet-derived g
31	120.5	6.5	275	2	JC6506	tumor necrosis fac
32	118.5	6.4	276	2	A47290	TSG-6 homolog p54
33	114.5	6.2	148	2	D49530	16k vascular endot
34	114.5	6.2	241	1	PFH02	platelet-derived g
35	112.5	6.1	200	2	I51551	platelet-derived g
36	112.5	6.1	215	2	S08220	platelet-derived g
37	112.5	6.1	226	2	I51550	platelet-derived g
38	111.5	6.0	319	2	I51569	UVS-2 protein - Af
39	110.5	5.9	2403	2	A59386	banko - human
40	110	5.9	166	2	JN0248	platelet-derived g
41	109	5.9	197	2	S25096	platelet-derived g
42	108.5	5.8	226	1	TYMVGS	PDGF-related trans
43	108	5.8	196	2	A37359	platelet-derived g
44	104.5	5.6	232	2	A41551	platelet-derived g
45	104	5.6	196	2	B28964	platelet-derived g

ALIGNMENTS

RESULT 1									
UC7591									
spinal cord-derived growth factor-B precursor - human									
C:Species: Homo sapiens (man)									
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001									
C:Accession: UC7591									
R:Hamada, T.; Ue-Tai, K.; Imaki, J.; Miyata, Y.									
Biochem. Biophys. Res. Commun. 280, 733-737, 2001									
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C									
A:Reference number: UC7591; PMID:21092670; PMID:11162582									
A:Accession: UC7591									
A:Molecule type: DNA									
A:Residues: 1-370 <HAM>									
A:Cross-references: DDBJ:AB033832									
C:Genetics:									
A:Gene: scdGF-B									
F:1-17/Domain: secretory signal sequence #status predicted <SIG>									
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>									
F:152-170/Region: CUB domain #status predicted									
F:1272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gro									
F:1294-308/Region: conserved motif #status predicted									
Query Match									
Best Local Similarity 40.0%; Score 742.5; DB 2; Length 370;									
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;									
QY	3	LEGLLVTSALAGQRGRGTQAESNLTKRFQSSN--KEONGVOD-POHERITVTNGSI	58						
DB	5	IFVYTLICANFCSCGRDTSATFQASIKALRNANLRBESNLTLDLYRDEITQKNGYV	64						
QY	59	HSPPPHPTYPNTLVLRVAEENWMIQLTDERFGLDEDDICKYFVEVEPSDGT	118						
DB	65	QSPFPNPSYPRNLLTLTFLHS-QENTRIQLVFDNQGLEAENDICRYDFEVEDIS	123						
QY	119	--IIGRWGSGCTVCGKQISKGNQIRIRFVSGVEPSPRGPCIHINIMVQPTAV----	171						
DB	124	TIIRGWRGKHGKVPRIKSRNQIKITKFSDDYVAVAGFEITYSL-LDDQPAASSTN	182						
QY	172	-----SPGVLPSPALPLDLNNAITAFSTLEDLIRYLPERRQLLEDLYR	217						
DB	183	WESTSSISGVSNVSPVTDPT-LIADALDKKIAEFPTVEDLLKFPNBSQEDLENNYL	241						
QY	218	PTWOLGKAIFYGKRSRVVDNLITTEVRVLYSCTPRNFSVIRELKTDTTIPMGCLLV	277						
DB	242	DTPEYRGRSY-HSRKSK-VLDRLINDAKYSCTPRNYSVIRELKLAVVFPFRCILV	299						
QY	278	KRCGNGACCLAHNGECQVPSKYTKKRYHYVQLQRP---KTVGVLKSKSLDVALEHHEE	334						
DB	300	QRCGNGCGCTVNRSCNSGSKTVKRYHEVLPBPGHIRKRGAKTMALVDIOLDHHR	359						
QY	335	CDVCV 339							

Db 360 CDCIC 364

RESULT 2

JC7998

platelet-derived growth factor-D - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003

C/Accession: JC7998

R/Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Laeky, J.A.

Biochem. Biophys. Res. Commun. 308, 126-132, 2003

A/Title: A novel murine PDGF-D splicing variant results in significant differences in p

A/Reference number: JC7998; PMID:12890490

A/Accession: JC7998

A/Molecule type: mRNA

A/Residues: 1-370 <ZHU>

C/Comment: This protein is a potent mesenchymal cell mitogen and chemottractant involve

C/Genetics:

A/Gene: pdgfr-D

A/Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2

C/Keywords: fibrosis; PDGF-D

Query Match 39.7%; Score 737.5; DB 2; Length 370;

Best Local Similarity 44.0%; Pred. No. 2.4e-56;

Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;

Db 16 QRRGTOAESNLSSKFOSSNKEQNGVOD-PQHERITVSTNGSIHSRPFPTYPRTVLY 74

26 QRSIKALRANR-----RDESNHLDLYORENIGVTSNGHVQSRFPNSYPRNLLT 80

Db 75 WRLVAENVWVLTPTDERFGLDEPDDEICKYDFVEVEBPSDGT--ILGRWGSSTVPCK 132

81 WMLRS-OEKRIOLDSFHQFGLAEANDICRYDFVEVEBSESSVTVGRGCHKELPPR 139

Db 133 QISKGQIRIRFVSDPESEPCIHYNVMPQFTAV-----SPS 174

140 ITRTQIKITFKSDDFVAKPGFKIYSFVEDPQPAASSETWSESVTSFGVSYHSPS 199

Db 175 VLPSPALPLDNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSR 234

200 ITDPT-LTDALDKTVAEPFTVEDLKHFPVSMQDLELYDTPIYRGRSY-HRKRK 257

Db 235 VVDNLITVEVRLVYSCPRNFSVIRELKRITPTIPGCLLYKRCGNCACCLHNCNC 294

258 -VDLDRLNDLVKYSCTPRNHSVNLBELKLITNAVFPRCLIVQRCGNGCGCTVWVWKC 316

Db 295 QCVPSKVTKKYHEVLTOLRP---KTGVRGLHKSITDVALHNEBCDVC 339

317 TCSSGKTVKKYHEVLTOLRP---KTGVRGLHKSITDVALHNEBCDVC 364

RESULT 3

JC7592

spinal cord-derived growth factor-B precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001

C/Accession: JC7592

R/Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A/Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/

A/Reference number: JC7591; PMID:21092670; PMID:11162582

A/Accession: JC7592

A/Contents: Fetal brain

A/Molecule type: mRNA

A/Residues: 1-370 <HAM>

A/Cross-references: DDBJ:AB052170

C/Genetics:

A/Gene: scdgb-B

F/1-17/Domain: secretory signal sequence #status predicted <Sig>

F/18-370/Product: spinal cord-derived growth factor-B #status predicted <Mat>

F/52-170/Region: CUB domain #status predicted

F/272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow

F/294-308/Region: conserved motif #status predicted

Query Match 39.6%; Score 736; DB 2; Length 370;

Best Local Similarity 45.6%; Pred. No. 3.3e-56;

Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

Db 37 EQNGVOD-PQHERITVSTNGSIHSRPFPTYPRTVLYWRLVAENVWVLTPTDER 95

42 ESNHLDLYRREINIVTGTGHVQSRFPNSYPRNLLTWRHLS-OEKRIQLAFPHQFG 100

Db 96 LEDPEDDICKYDFVEVEBPSDGT--ILGRWGSSTVPCKQISKGQIRIRFVSDPE 153

101 LBEANDICRYDFVEVEBSESSVTVGRGCHKELIPITRTQIKITFGSDDFVAK 160

Db 154 PGFCIHYNIV--MPOFTAV-----SPSVLPSPALPLDNLNNAITAFST 195

161 PGKIYSPVEDPQPAASEIMWSEVTSFGVSYHSPVW-DSTLTADALDKAIAEPDI 219

Db 196 LEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDNLITVEVRLVYSC 255

220 VEDLIRYFNPASWQDLEMLYMDTPRYGRSY-HERKSR-VLDRLNDLVKYSCTPRN 277

Db 256 SVSIRELKRITPTIPGCLLYKRCGNCACCLHNCQCVPSKTKYHEVLTOLRP-- 313

278 SVNLREELKLITNAVFPRCLIVQRCGNGCGCTVWVWKCCTSSGKTVKKYHEVLT 337

Db 314 -KTGVRGLHKSITDVALHNEBCDVC 339

338 FKRGKAKMALVDTQDLHNEBCDVC 364

RESULT 4

T09456

intrinsic factor-B12 receptor Cubilin precursor - human

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002

C/Accession: T09456

R/Kozyraki, R.; Kristiansen, M.; Slahteroglu, A.; Hansen, C.; Tommerup, P.

Blood 91, 3593-3600, 1998

A/Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteri-

ion.

A/Reference number: Z16677; PMID:98241400; PMID:9572993

A/Accession: T09456

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-3623 <KOZ>

A/Cross-references: EMBL:AF034611; NID:G3929528; PID:AA082612.1; PID:G3929529

C/Genetics:

A/Map position: 10p12

C/Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C/Keywords: receptor; vitamin B12 uptake

F/1-24/Domain: signal sequence #status predicted <Sig>

F/25-3623/Product: intrinsic factor-B12 receptor #status predicted <Mat>

F/436-467/Domain: EGF homology <EGF>

Query Match

Best Local Similarity 9.8%; Score 183; DB 2; Length 3623;

Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

Db 19 GQAEENLSSKQF-----SNKEQNG-----VDPQHERITVSTNGSIHSRPF 65

892 GDIDPFIITSYVNFVTFVKSSSTENHFMKAFSAEDACCEIITEST-GTIQSGHGN 950

Db 66 TYPRNTVLAWRVAENVWVLTPTDERFGLDEPDDEICKYDFVEVEBPSDGTILGRWG 125

951 VYPHGINCTWHL-VQPNHLILMF-ETHLHFNHN--CTNDYLEVYDSDSTSLGRYCG 1006

Db 126 SCTVPEKQISKGQIRIRFVSDPESEPCIHYNIV-----MPOFTAVSPVLPSP 179

1007 K-SIPPSLSSGNSLMLVVTSDLAWE-GFLINVEAIAATACIDYTDIDGTFRSP-- 1062

Db 180 ALPLDNLNNAITAFSTLEDLIRYLEPERWQDLEDLYR--PTWQLGKAFVGRKSRV 236

1063 ---NFPNN-----YPNWV---ECIYRITVGTGLIAVFTNFSLEAI 1099

QY 237 DLNLTRE--EVR-----LY--SCTPRNFVSIREBK-RDTT-----FM 271
 DB 1100 G-NYTFLELRDGYEKSPLLGIFYSNNLPPTIISHNNKMLKMLKSFQDITRSGFSAYW 1158
 QY 272 PGCLLVKRCGNGACACCHNCCEOCVPSKVTKKYHE---VLQLRPKGVRLGHSRLNDVA 328
 DB 1159 DGS--STGCCGN-----LTTSGGTISIRPYMPYTHSSECTYWLKSSHC-SAFELRFDHF 1211
 QY 329 LEHHEEC 335
 DB 1212 LEHHPNC 1218
 RESULT 5
 BMH01
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
 N:Alternate names: bone morphogenic protein 1 (BMP1)
 C:Species: Homo sapiens (man)
 C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C:Accession: A37278; E58788
 R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072730; PMID:3201241
 A:Accession: A37278
 A:Molecule type: mRNA
 A:Residues: 1-730 <WQ2>
 A:Cross-references: GB:M2488; NID:G179499; PIDN:AAA51833.1; PID:G179500
 C:Genetics:
 A:Gene: GDB:BMP1
 A:Cross-references: GDB:125203; OMIM:112264
 A:Map position: 8p21-8p21
 C:Function:
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C:Superfamily: procollagen C-endopeptidase; aspartic homology; Ctr/Cis repeat homology; B
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
 F:1-22/Domain: signal sequence #status predicted <sig>
 F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
 F:130-321/Domain: aspartic homology <Asp>
 F:322-431/Domain: Ctr/Cis repeat homology <CTR2>
 F:435-544/Domain: Ctr/Cis repeat homology <CTR1>
 F:551-587/Domain: EGF homology <EGF>
 F:551-700/Domain: Ctr/Cis repeat homology <CTR3>
 F:91,142,332,363,599/Binding site: carbonylcarboxylate (Asn) (covalent) #status predicted
 F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:214/Active site: Glu #status predicted
 F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 Query Match 9.8%; Score 181.5; DB 1; Length 730;
 Best Local Similarity 37.3%; Pred. No. 1.4e-07;
 Matches 50; Conservative 20; Mismatches 47; Indels 17; Gaps 7;
 QY 55 NGSTHSRPHPTVRYNTVLVRLVA--VEENWIDLTDERGLEDPPDDICKDPFVVEE 113
 DB 599 NGSTHSRPHPTVRYNTVLVRLVA--VEENWIDLTDERGLEDPPDDICKDPFVVEE 653
 QY 114 --PSDGTILGRMGSGTVPGKQISKGNQIRIRFVSDEVPSPGCTHYNTVMQFTEAV 171
 DB 654 GLTADSLTKHGKFGCS -EKPEVITISQYNNMVFESKSDMTV-SKKGFKAHF-----FSBK- 704
 QY 172 SPSTVLPSPALPLDL 185
 DB 705 RPAALQPRGRPHQL 718
 RESULT 6
 JQ0948
 A5 antigen precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: JH0466; JQ0948

R:Takagi, S.; Hirata, T.; Agata, K.; Mochi, M.; Eguchi, G.; Fujisawa, H.
 Neuron 7, 295-307, 1991
 A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
 A:Reference number: JH0466; MUID:91337458; PMID:1908252
 A:Accession: JH0466
 A:Molecule type: mRNA
 A:Residues: 1-927 <TAK>
 A:Cross-references: GB:D10467; GB:D01077; NID:q222962; PIDN:BA01260.1; PID:q222963
 A:Experimental source: tadpole, brain
 A>Note: This protein has motifs homologous to complement components C1r and C1s and to
 C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal re
 C:Superfamily: Xenopus A5 antigen; Ctr/Cis repeat homology; discoidin I amino-terminal
 C:Keywords: duplication; glycoprotein; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <sig>
 F:22-927/Product: A5 antigen #status predicted <Asn>
 F:27-138/Domain: Ctr/Cis repeat homology <CTR1>
 F:147-262/Domain: Ctr/Cis repeat homology <CTR2>
 F:274-424/Domain: discoidin I amino-terminal homology <DN1>
 F:430-584/Domain: discoidin I amino-terminal homology <DN2>
 F:646-812/Domain: MAM homology <MAM>
 F:861-883/Domain: transmembrane #status predicted <TM>
 F:150,261,300,523,844/Binding site: carbonylcarboxylate (Asn) (covalent) #status predicted
 Query Match 9.7%; Score 179.5; DB 1; Length 927;
 Best Local Similarity 31.6%; Pred. No. 2.9e-07;
 Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;
 QY 50 ITWSTNGSIHSPRPHPTVRYNTVLVRLVA--VEENWIDLTDERGLEDPPDDICKDPFV 109
 DB 31 IKTSPEYLSAGVPHSPGSCEMLIQAPBHQRIMINPNPFLDEDE--CKTDYV 87
 QY 110 EV--EESDGTILGRMGSGTVPGKQISKGNQIRIRFVSDEVPSPGCTHYNTVMQFTEAV 165
 DB 88 EVIDGDMAQQLGKCKGK-IAPSPVSTSPSIFIRFVSDEVPSPG-AGFIRFVFPKTP 145
 QY 166 ----QPTFA--VSPSTVLPSPALPLDLNNAITVASTLEDIRYDEPRWOLDIE 213
 DB 146 EGSNFTSNQGVKSPKPYRKPALAECTYIIRAPKQETV--LEFSFLEAD 197
 RESULT 7
 JQ2218
 procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
 N:Alternate names: bone morphogenic protein 1
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
 C:Accession: JQ2218
 R:Meno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Xung, H.
 Gene 134, 257-261, 1993
 A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prot
 A:Reference number: JQ2218; MUID:94085787; PMID:8262384
 A:Accession: JQ2218
 A:Molecule type: mRNA
 A:Residues: 1-707 <MAE>
 A:Cross-references: GB:J12249; NID:q406540; PIDN:AA16313.1; PID:q406541
 A:Comment: This protein induces ectopic cartilage formation in vivo.
 C:Superfamily: procollagen C-endopeptidase; aspartic homology; Ctr/Cis repeat homology;
 C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
 F:93-284/Domain: aspartic homology <Asp>
 F:285-397/Domain: complement 1r/1s-like repeat
 F:398-510/Region: Ctr/Cis repeat homology <CTR1>
 F:398-510/Region: complement 1r/1s-like repeat
 F:398-510/Region: Ctr/Cis repeat homology <CTR2>
 F:514-550/Domain: EGF homology <EGF>
 F:554-666/Region: complement 1r/1s-like repeat
 F:554-666/Domain: Ctr/Cis repeat homology <CTR3>
 F:62,105,295,326/Binding site: carbonylcarboxylate (Asn) (covalent) #status predicted
 F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:177/Active site: Glu #status predicted
 F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 Query Match 9.5%; Score 176; DB 2; Length 707;
 Best Local Similarity 43.3%; Pred. No. 4.2e-07;

J. Biol. Chem. 269, 32572-32578, 1994

A>Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (wTld) are encoded by two genes in the mouse genome.

A.Reference number: A58788; PMID:95096114; PMID:7798260

A.Molecule type: mRNA

A.Residues: 703-986 <TAk>

A.Cross-references: GB:IJ5279; NID:g619860; PIDN:AAC41710.1; PID:g619861

C.Genetics:

A.Gene: GDB:BMP1; BMP-1

A.Cross-references: GDB:I25203; OMIM:112264

A.Map position: 8p21-8p21

C.Function:

A.Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I C-suprafamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; E Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; glu F.1-22/Domain: signal sequence #status predicted <SIG>

F.23-986/Product: procollagen C-endopeptidase tollold-like splice form #status predicted F.130-321/Domain: astacin homology <AST>

F.132-431/Domain: Clr/Cls repeat homology <CLR1>

F.1435-544/Domain: Clr/Cls repeat homology <CLR2>

F.1551-587/Domain: EGF homology <EGF1>

F.1591-700/Domain: Clr/Cls repeat homology <CLR3>

F.107-742/Domain: EGF homology <EG2>

F.1747-856/Domain: Clr/Cls repeat homology <CLR4>

F.1860-973/Domain: Clr/Cls repeat homology <CLR5>

F.191,142,332,363,559/Binding site: carbonyl/deate (Asn) (covalent) #status predicted F.163-319,185-205,328-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-666 F.213,217,223,273/Binding site: zinc (His, His, His, Tyr) #status predicted F.214/Active site: Glu #status predicted F.165,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.1%; Score 169; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 2.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Oy 55 NGSIHSRPFHTYRNVLVRLVA--VEENWIOGLTPDRFGLEBDEDDICKDFVEVER 113
|||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||
Db 599 NGSITSGWEKEPEPPNNKCMQLVAPTYRISLQDFETEG---NDVCCKDPEVENS 653

Oy 114 --PSDGILRWCGSGTVPGKOISKNGDIRIRFVDEVPSPGFCIH 160
|||:::||||:::||||:::||||:::||||:::||||:::||||:::||||
Db 654 GLTRDSLTKHKPCGS-EKPEVITSQYNMRVFEKSDNTV-SKKGRANF 700

RESULT 11

I49540

procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollold-like splice form - mouse

C.Species: Mus musculus (house mouse)

C.Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 21-Jan-2000

C.Accession: I49540

F.Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994

A.Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is related to Drosophila decapentapeg repeats.

A.Reference number: I49540; MUID:94229342; PMID:8174772

A.Accession: I49540

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1-991 <RSS>

A.Cross-references: GB:I24755; NID:g439606; PIDN:AA37306.1; PID:g439607

C.Genetics:

A.Gene: Bmp-1

C.Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; E Keywords: hydrolase; metalloproteinase; zinc

F.135-326/Domain: astacin homology <AST>

F.556-592/Domain: EGF homology <EG1>

F.596-705/Domain: Clr/Cls repeat homology <CLR>

F.712-747/Domain: EGF homology <EG2>

F.18,222,228,271/Binding site: zinc (His, His, His, Tyr) #status predicted F.219/Active site: Glu #status predicted

Query Match 9.1%; Score 169; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 2.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

```

Oy 55 GSGHSRPRPHPTYPENTLVLRVLA-VBENWIDQLTDFPERGLDPEDDICXDPFVBE 113
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 604 NGSTISPEWPEYPPNKKNCIKWLVAPTQYRISLQDPDEFETEG----NDVCKDPFVEVS 658

Oy 114 --PSDGTILGRWCGSGTVPGRKQISKGNQIRIRFVSDEYFSPSPGFCIH 160
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 659 GLTADSKLHGKFCDS-EKREVITISQYNNMRREFPSDNTV-SKKGFKAHF 705

RESULT 12
A55362
procollagen I C-proteinase enhancer protein precursor - human
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C/Accession: A55362
R.Takahara, K.; Kessler, E.; Bliniaminov, L.; Brussel, M.; Eddy, R.L.; Jani-Sait, S.; Sho
J. Biol. Chem. 269, 26280-26285, 1994
A>Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification,
A.Reference number: A55362; MUID:95014462; PMID:7523404
A.Accession: A55362
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-449 <TAK>
A.Cross-references: GB:LJ3799; NID:G642907; PIDN:AAA61949.1; PID:G642908
C/Genetics:
A.Gene: GDB:PCOLCE
A.Cross-references: GDB:305468; OMIM:600270
A.Map position: 7q21.3-7q22
C/Superfamily: C1r/C1s repeat homology
C/Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F.1-25/Domain: signal sequence #status predicted <MAT>
F.325-449/Product: #status predicted <MAT>
F.327-146/Domain: C1r/C1s repeat homology <C1R1>
F.159-270/Domain: C1r/C1s repeat homology <C1R2>
F.126/Modified site: pyrolysine carboxylic acid (Gln) (in mature form) #status predicted
F.129/431/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 154; DB 2; Length 449;
Beet Local Similarity 33.8%; Pred. No. 1.9e-05;
Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;

Oy 56 GSHSRPRPHPT-YRNTVLVRLVAVEENWMIQLTFDERFGLDPEDDICXDEVEV--- 111
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 168 GTLTTPMNPESDYPFGISCSWHIIAPPQV-IALT-F-EKFLF--PDYCKYDSVSPNG 223

Oy 112 EEPDGTILGRWCGSGTVPGRKQISKGNQIRIRFVSDEYFSPSPGFCIHYNIVMPOFT-- 168
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 224 AVSDSRIRIGKFCGP-AVPGSISEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKB 280

Oy 169 -----EAVSPSV-LPPSALP 182
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 281 GQGPGRKRGTEPKVLPKPSQP 302

RESULT 13
A39288
dorsal-ventral patterning protein tollid (EC 3.4.24.-) - fruit fly (Drosophila melanog
C/Species: Drosophila melanogaster
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A39288
R.Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A>Title: The Drosophila dorsal-ventral patterning gene tollid is related to human bone
A.Reference number: A39288; MUID:92034970; PMID:1840509
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-1057 <SHI>
A.Cross-references: GB:M76976; NID:G157305; PIDN:AAA28491.1; PID:G157306
C/Genetics:
A.Gene: flyBase:clid
A.Cross-references: flyBase:FBgn0003719

```

C/Superfamily: dorsal-ventral patterning protein tollid; astacin homology; C1r/C1s repd
 C/Keywords: duplication; hydrolase; metalloproteinase; zinc
 F/136-329/Domain: astacin homology <AST>
 F/352-464/Domain: C1r/C1s repeat homology <C1R1>
 F/468-578/Domain: C1r/C1s repeat homology <C1R2>
 F/585-620/Domain: EGF homology <EG1>
 F/624-740/Domain: C1r/C1s repeat homology <C1R3>
 F/747-782/Domain: EGF homology <EG2>
 F/787-896/Domain: C1r/C1s repeat homology <C1R4>
 F/900-1013/Domain: C1r/C1s repeat homology <C1R5>
 F/221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
 F/222/Active site: Glu #status predicted

Query Match

Best Local Similarity 8.0%; Score 148.5; DB 1; Length 1057;
 Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;

QY 50 ITVSTNGSHSPRPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEE 109
 Db 472 LKTKQSDSPVPMYDMPDKCWCWRTA-PNNHQVAKF-QSFLE-KHDGCAVDFV 527

QY 110 EVEE--PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 147
 Db 528 EIRDGNHSDSRLLGRFGDKLPNIK-TRSNQWYIRFVSD 566

RESULT 14

A59271

Ra-reactive factor (EC 3.4.21.-) 2 precursor - human

N/Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)

C/Species: Homo sapiens (man)

C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000

C/Accession: A59271

R/Title: S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laureen, S.B.; Poulsen, K.

Nature 386, 506-510, 1997

A/Title: A second serine protease associated with mannan-binding lectin that activates C

A/Reference number: A59271; MUID:97242412; PMID:9087411

A/Accession: A59271

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-686 <JEN>

A/Cross-references: GB:Y09926; NID:94007626; PIDN:CAAT1059.1; PID:94007627

A/Experimental source: tissue liver

A/Note: Submitted to GenBank, December 1996

A/Note: parts of this sequence, including the amino end of the mature protein, were dete

C/Genetics:

A/Gene: GDB:MASP2

A/Cross-references: GDB:6071500

A/Map position: lp36.2-lp36.3

C/Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H

C/Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>

F/19-134/Domain: C1r/C1s repeat homology <C1R1>

F/142-180/Domain: EGF homology <EGF>

F/184-293/Domain: C1r/C1s repeat homology <C1R2>

F/300-361/Domain: complement factor H repeat homology <FH1>

F/366-430/Domain: complement factor H repeat homology <FH2>

F/445-679/Domain: trypsin homology <TRY>

F/72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,

F/158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F/444-445/Cleavage site: Arg-116 (autolytic) #status predicted

F/483,532/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 7.7%; Score 143.5; DB 1; Length 686;
 Matches 34; Conservative 25; Mismatches 42; Indels 5; Gaps 4;

QY 55 NSGSHSPRPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEE 114

Db 193 SGELSPPEYRPPKSSCYTS-ISLEBGSVLDFESFDVTHPETLCRYDFLKIQ-- 249

QY 115 SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPSPGFCIHY 160

Db 250 TNEEHGPPCGK-TLPHRIETKSNVTITFVDE-SGHTGKIMHY 293

RESULT 15

T31069

collid-BMP-1 like protein 1 - California sea hare

N/Alternate names: probable metalloprotease Tbl-1

C/Species: Aplysia californica (California sea hare)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000

C/Accession: T31069

R/Title: Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; E.

U. Neurosci. 17, 735-764, 1997

A/Title: A developmental gene (Tollid/BMP-1) is regulated in Aplysia Neurons by treatm

A/Reference number: Z20965; MUID:98007484; PMID:8987797

A/Accession: T31069

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1070 <LID>

A/Cross-references: EMBL:U57369; NID:91899041; PID:91899042; PIDN:AAC47485.1

C/Superfamily: dorsal-ventral patterning protein tollid; astacin homology; C1r/C1s rep

Query Match

Best Local Similarity 7.5%; Score 139.5; DB 2; Length 1070;
 Matches 70; Conservative 36; Mismatches 102; Indels 11; Gaps 17;

QY 56 GSISHSPRPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEE 112

Db 529 GFINSFAYVDEGSDKVCNM-VITREGVQVLAEPFTFTEF---DPD---CAYDVEIR 581

QY 113 --EPDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPSPGFCIHY----- 160

Db 582 DGDGTQSPVGVYCGTTR-PPNAISTSRHLVYKVFVSDISM-QKGSFASYLEVEDECE 639

QY 161 -----NIMWQFTEAVSPV 175

Db 640 DHGCEHVCAVNTIGSECTKIGIELHSDKCKEACGYLDAPSGTISPSF-----PDL 694

QY 176 LPPSALPLDLNNATPFS---TLEDLIRYLEPERMQLDLDLYRPTWLLGKAFVG 230

Db 695 YPPD-----KNCVHISAPKSHLTITVFTHMDL-WMGDECEL-----DFVRVTVVG 741

QY 231 KRSRVVDLNLTEEVRLYSCTPRNSVS--TEBELKRTDTITWPGCLL-----VKRCGN 283

Db 742 NKER-----LOGQYCGFMAPPSITSLSNLRIFRSDDTLTKTGFSPMDYVADVDECASS 795

QY 284 CACCLHNCN-----ECOC 296

Db 796 NGGCKHICENTVGSFHCSC 814

Search completed: May 27, 2004, 15:47:22
 Job time : 15 secs

DR	PROSITE; PS01180;	CUB; 2.
DR	PROSITE; PS01285;	FA58C_1; 2.
DR	PROSITE; PS01286;	FA58C_2; 2.
DR	PROSITE; PSS0022;	FA58C_3; 2.
DR	PROSITE; PS00740;	MAM_1; 1.
DR	PROSITE; PSS0060;	MAM_2; 1.
KW	Angiogenesis; Transmembrane;	Glycoprotein; Neutrone; Signal; Repeat;
KW	Receptor; Antigen.	
FT	SIGNAL	1
FT	CHAIN	21
FT	DOMAIN	22 928
FT	DOMAIN	22 860
FT	TRANSMEM	861 883
FT	DOMAIN	884 928
FT	DOMAIN	27 141
FT	DOMAIN	147 265
FT	DOMAIN	275 424
FT	DOMAIN	431 584
FT	DOMAIN	646 812
FT	DISULFID	27 54
FT	DISULFID	82 104
FT	DISULFID	147 173
FT	DISULFID	206 228
FT	DISULFID	275 424
FT	DISULFID	431 584
FT	CARBOHYD	150 150
FT	CARBOHYD	261 261
FT	CARBOHYD	300 300
FT	CARBOHYD	523 523
FT	CARBOHYD	844 844
QO	SEQUENCE	928 AA; 103416 MW; A6B323BDAA4789D CXC64;

Query Match	9.7%;	Score 179.5;	DB 1;	Length 928;
Best Local Similarity	31.6%;	Pred. No. 2.2e-07;		
Matches 55;	Conservative 29;	Mismatches 73;	Indels 17;	Gaps 7

QY 50 ITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWIIQTLFERFGLEDPEDDICKYDFV 109

110 EV--EPPSDGTLIGRWGSGSTVPGKOISKGNQIRIREVSDPEYPPSEPFGCIHNYLMP-- 165

Db 88 EVIDGMANGQLLEKRYCGK-IAPSEPLVSTGPSIFIRFVSDYETPG-AGPSIRYEVEFKTGP 145

```
QY      166 ---QFEFA--VSPSVLPSPALPLDLINNAITAFSTIEDLIRYLEPEKWOJDE 213
```

DU 110 BCKNFI ISSNGVLSFNIENIENALCEI111FAFMUQELV--LNFESFEUEAD 19/

```

RESULT 2
BMP1_XENLA
-----

```

AC P98070;
DT 01-FEB-1996 (Rel. 33, Created)

DE Base morphological variants 1 occurrence (ID 3 4 34) (run 1)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DT 01-FEB-1996 (Rel. 33, last sequence update)
DI

05 Xenopus laevis (African clawed frog).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

0X Xenopodinae; Xenopus.
NCBI TaxID=8355:
0C amphibia; batraciata; anura; mesobatrachia; figipnea; figipnae;
0C xenopodinae; xenopus.

RN [1]
RP SEQUENCE FROM N.A.
SC

RX MEDLINE=94085787; PubMed=8262384;
RA Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.

RT morphogenetic protein-1 during early embryonic development."; Gene 134:257-261 (1993)

CC -I- FUNCTION: Involved in pattern formation in gastrula and later differentiation of developing organs.

cc. tadpoles; little or no expression in morula and late gastrula.

CC -1 SIMILARITY: Belongs to peptidase family M12A.
CC -1 SIMILARITY: Contains 1 BGF-like domain.
CC -1 SIMILARITY: Contains 3 CUB domains.
CC -----
CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the Max Institute of Molecular Biology and Biophysics, Heidelberg, Germany.

CC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

 or send an email to license@ib-sib.ch.

DR EMBL; L12249; AAA16313.1; -.
DR PIR; JC2218; JC2218.

DR MEROPS; M12.005; -.
DR InterPro; IPR000152; Asx hydroxyl S.

DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF Ca.
InterPro; IPR006200; EGF_1; bc
DB

DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.

DR PF08431; CUB: 3.
Pfam: PF01400; Astacin, 1.

DR Plam; PF000008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
CHART SW000000; CPM 1

DR	SMART; SM00179; EGF_CA; 1.
DR	SMART; SM00235; ZnMC; 1.

DR PROSITE; PS00010; ASA_HYDROXYL, 1.
DR PROSITE; PS01180; CUB, 3.
DR PROSITE; PS00022; EGF_1; FALSE NEG
RR

```
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
```

DR PROSITE; PS00142; ZINC_PROTEASE, 1.
KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;

	1	2	POTENTIAT
KW	Hydroxylase; Protease;	Metalloprotease; Egr-like domain;	zinc; calcium;
Signal.			
STGNAI			
STGNAI			

FT	PROPEP	?	83	POTENTIAL.
FT	CHAIN	84	707	BONE MORPHOGENETIC PROTEIN 1.

[illegible]

FT	DOMAIN	EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
510	551	
554	666	
554	666	CUB 3.
MEMIT	127	FTING (CONSTRUCTED) (BY CUB3/FTING)
127	127	

FT ACT SITE	177	177	BY SIMILARITY.
FT METAL	180	180	ZINC (CATALYTIC) (BY SIMILARITY).

FT	MEAL	186	186	ZINC (CAIADHIC) (BI SIMILARITY).
DISULEID	146	149		BY SIMILARITY.
DISULEID	514	526		BY SIMILARITY.

FT	DISULFID	522	535	BY SIMILARITY.
FT	DISULFID	537	550	BY SIMILARITY.

[illegible]

SEQUENCE	70-73	00077	WM	1870000017	000000	00004
CARBOHYD	562	562	N-LINKED	(GLCNAC. . .)	(POTENTIAL).	
FT	326	326	N-LINKED	(GLCNAC. . .)	(POTENTIAL).	
FT	326	326	N-LINKED	(GLCNAC. . .)	(POTENTIAL).	

Query Match 9.58; Score 176; DB 1; Length 707;

Best local similarity 42.3%; Fied. NO. 3.1E-07/
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

```
OY      ||| : | | : | | | | |  
55 NGSIHPRFHTPTVLRVAENBNWQLTDERFGJEDPEDDICKDFVEEVB- 113  
OZ      ||| : | | : | | | | |
```

114 -PSDGTILGRWCGSTVPGKQISKGNQIRIRFVSDVYPSSEBGF 156

[illegible]

Db 618 LTSDSKLHGKFGS-ELPAVITSOYNNMRIFKSDNTV-SKGF 659

RESULT 3
 ID SPAN_STRPU STANDARD; PRT; 616 AA.
 AC P98068;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SPAN protein precursor (EC 3.4.24.-).
 GN SPAN.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidae; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 ON NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92315921; PubMed=1618141;
 RA Reynolds S.D., Angerer L.M., Pails J., Nasir A., Angerer R.C.;
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of
 RT sea urchin embryos, include one encoding a protein related to tollid
 RT and BMP-1."
 RL Development 114:769-786(1992).
 CC -1- TISSUE SPECIFICITY: Asymmetrically along the animal-vegetal axis
 CC of the blastula.
 CC -1- DEVELOPMENTAL STAGE: Very early blastula (between 16-cell stage
 CC and hatching).
 CC -1- SIMILARITY: Belongs to peptidase family M12A.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 2 CUB domains.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 CC EMBL; M84144; AAA30072.1; -.
 DR HSSP; P28825; 11AF.
 DR MEROPS; M12.013; -.
 DR InterPro; IPR000659; CUB.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001506; Peptidase_M12A.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00431; CUB; 2.
 DR PRINTS; PR00480; ASTACIN.
 DR SMART; SM0042; CUB; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM0235; ZmC; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;
 KW Metalloprotease; EGF-like domain; Signal.
 FT SIGNAL 1
 FT PROPEP 16
 FT CHAIN 93
 FT DOMAIN 94 616
 FT DOMAIN 89 93
 FT DOMAIN 94 295
 FT DOMAIN 295 329
 FT DOMAIN 340 450
 FT DOMAIN 451 502
 FT DOMAIN 503 614
 FT METAL 190
 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT SITE 191 191 BY SIMILARITY.
 FT METAL 194 194 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 200 200 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 299 315 BY SIMILARITY.
 FT DISULFID 305 317 BY SIMILARITY.
 FT DISULFID 319 328 BY SIMILARITY.
 SQ SEQUENCE 616 AA; 67902 MW; 397CD923FFB9EB98 CRC64;
 Query Match 9.3%; Score 173.5; DB 1; Length 616;
 Best local Similarity 27.08; Pred. No. 4.2e-07;
 Matches 70; Conservative 33; Mismatches 93; Indels 63; Gaps 14;
 Oy GSISPPFPPTPTPTVTLVRLVAVENWVQLTLPDRFGLEDPEEDICKYDFEVEBPS 115
 Db 349 GEISPPFPPTPTPTVTLVRLVAVENWVQLTLPDRFGLEDPEEDICKYDFEVEBPS 115
 Oy 116 DGTILGRCGSGVTPGQISKNGQIRIRFVSDEYFS--EPGCIHYNIYMPQTEAVSP 173
 Db 405 INSIGERFCGN-TLPVQISSNQMWVSFTSD--PSITRRGFATVVIIL-QTTVFST 459
 Oy 174 SVL---PPSALPDLNNAITASTEDLIRYLEPERKQDLBRLVPTWOLGKAFVFG 230
 Db 460 TTTQTTPPTSTTTTQTTPSTTTTQT-----TNPSTTTTQTD--TPVIGSCGQTFV-G 509
 Oy 231 RKSRLVDLNLTEBRLVYCTPRNFSYSIR-----EELKRPDTIP-----W 271
 Db 510 VEGRVASPNV-----PNDYDNLQCDVYIEVDGRVRLTEDEGLBDETTCTRW 558
 Oy 272 PGCLL-----VKRCG 281
 Db 559 DSLMINNGIKVGMKMG 577

 RESULT 4
 ID BMPI_HUMAN STANDARD; PRT; 986 AA.
 AC P13497; Q13292; Q14874; Q99421; Q99422; Q99423; Q99424;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
 DE (Procollagen C-proteinase) (PCP) (Mammalian tollid protein) (MTld).
 GN BMPI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BMPI-3).
 RC TISSUE=Skin;
 RX MEDLINE=96209868; PubMed=8643539;
 RA Li S.W., Sieron A.L., Petrala A., Hojima Y., Arnold W.V.,
 RA Prockop D.J.;
 RT "The C-proteinase that processes procollagens to fibrillar collagens
 RT is identical to the protein previously identified as bone morphogenic
 RT protein-1."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BMPI-1).
 RX MEDLINE=69072730; PubMed=3201241;
 RA Worney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,
 RA Kriz R.W., Hewick R.W., Wang B.A.;
 RT "Novel regulators of bone formation: molecular clones and
 RT activities."
 RL Science 242:1528-1534(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS BMPI-4; BMPI-5 AND BMPI-6).
 RC TISSUE=Placenta;
 RX MEDLINE=98160316; PubMed=9500680;
 RA Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
 RT "Three alternatively spliced variants of the gene coding for the human
 RT bone morphogenetic protein-1."
 RL J. Mol. Med. 76:141-146(1998).

[4] PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).
 RP TISSUE-Placenta; PubMed:7798260;
 RA Takahara K., Lyons G.E., Greenspan D.S.;
 RT "Bone morphogenetic protein-1 and a mammalian tollid homologue (mTld)
 RT are encoded by alternatively spliced transcripts which are
 RT differentially expressed in some tissues.";
 RL J. Biol. Chem. 269:32572-32578(1994).
 RN [5]
 RP DISULFIDE BOND IN METALLOPROTEIN DOMAIN.
 RX MEDLINE:21336528; PubMed:11283002;
 RA Garrique-Antar L., Barker C., Kadler K.E.;
 RT "Identification of amino acid residues in bone morphogenetic
 RT protein-1 important for procollagen C-proteinase activity.";
 RL J. Biol. Chem. 276:26237-26242(2001).
 CC -I- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
 CC and III. Induces cartilage and bone formation.
 CC -I- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
 CC Ala-|-Asp in type I and II procollagens and at Arg-|-Asp in type
 CC III.
 CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -I- ENZYME REGULATION: Activity is increased by the procollagen C-
 CC endopeptidase enhancer protein.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=7;
 CC Name=BMP1-3;
 CC IsoId=PI3497-1; Sequence=Displayed;
 CC Name=BMP1-1;
 CC IsoId=PI3497-2; Sequence=VSP_005461, VSP_005462;
 CC Name=BMP1-2;
 CC IsoId=PI3497-7; Sequence=Not described;
 CC Name=BMP1-4;
 CC IsoId=PI3497-3; Sequence=VSP_005463, VSP_005464;
 CC Name=BMP1-5;
 CC IsoId=PI3497-4; Sequence=VSP_005465, VSP_005466;
 CC Name=BMP1-6;
 CC IsoId=PI3497-5; Sequence=VSP_005467, VSP_005468;
 CC Name=BMP1-7;
 CC IsoId=PI3497-6; Sequence=VSP_005469, VSP_005470;
 CC -I- TISSUE SPECIFICITY: Ubiquitous.
 CC -I- SIMILARITY: Belongs to peptidase family M12a.
 CC -I- SIMILARITY: Contains 2 EGF-like domains.
 CC -I- SIMILARITY: Contains 5 CUB domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U50330; AAA93462.1; -
 CC EMBL: M22488; AAA51833.1; -
 CC EMBL: Y08723; CAA69973.1; -
 CC EMBL: Y08724; CAA69974.1; -
 CC EMBL: Y08725; CAA69975.1; -
 CC EMBL: L35278; AAC41703.1; -
 CC EMBL: L35279; AAC41710.1; -
 CC PIR: A37278; B58788.
 CC HSSP: P00736; IAPQ.
 CC MEROPS: M2.005; -.
 CC Genew: HGNC:1067; BMP1.
 CC MIM: 11264; -.
 CC GO: GO:0005576; C:extracellular; NAS.
 CC GO: GO:0008237; E:metalloproteinase activity; NAS.
 CC GO: GO:0001502; P:cartilage condensation; TAS.
 CC GO: GO:0007275; P:development; TAS.
 CC InterPro: IPR000152; Asx_hydroxyl_S.
 CC InterPro: IPR000859; CUB.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR006209; EGF_Like.
 CC

DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR006026; Peptidase_M12a.
 DR InterPro: IPR001506; Peptidase_M12a.
 DR Pfam: PF01400; Astacin; 1.
 DR Pfam: PF00431; CUB; 5.
 DR Pfam: PF00008; EGF; 2.
 DR PRINTS: PR00480; ASTACIN.
 DR SMART: SM00042; CUB; 5.
 DR SMART: SM00179; EGF_Ca; 2.
 DR SMART: SM00235; ZnMC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 2.
 DR PROSITE: PS01180; CUB; 5.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS00026; EGF_3; 2.
 DR PROSITE: PS01187; EGF_Ca; 2.
 DR PROSITE: PS00142; ZINC_PROTEIN; 1.
 DR Growth factor: Cytokine; Repeat; Osteogenesis; Chondrogenesis;
 KW Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; signal;
 KW Glycoprotein; Zymogen; Alternative splicing.
 FT SIGNAL 1 22
 FT PROPEP 23 120
 FT CHAIN 121 986
 FT DOMAIN 121 321
 FT DOMAIN 322 434
 FT DOMAIN 435 546
 FT DOMAIN 547 588
 FT DOMAIN 591 703
 FT DOMAIN 704 743
 FT DOMAIN 747 859
 FT DOMAIN 860 976
 FT METAL 213 213
 FT ACT_SITE 214 214
 FT METAL 217 217
 FT METAL 223 223
 FT DISULFID 183 186
 FT DISULFID 322 348
 FT DISULFID 375 397
 FT DISULFID 435 461
 FT DISULFID 488 510
 FT DISULFID 551 563
 FT DISULFID 559 572
 FT DISULFID 574 587
 FT DISULFID 591 617
 FT DISULFID 644 666
 FT DISULFID 707 718
 FT DISULFID 714 727
 FT DISULFID 729 742
 FT CARBOHYD 91 91
 FT CARBOHYD 142 142
 FT CARBOHYD 332 332
 FT CARBOHYD 363 363
 FT CARBOHYD 599 599
 FT VARSPLIC 703 730
 FT
 FT VARSPLIC 731 986
 FT
 FT VARSPLIC 245 302
 FT
 FT VARSPLIC 303 986
 FT
 FT VARSPLIC 589 622
 FT
 FT VARSPLIC 623 986
 FT
 FT VARSPLIC 703 717
 FT

AACGGTTTAKNGSITSPGPKKYPNNKCTIOLV -> GCY
 DIQVKGPLMDRCSTLSTHGPMLGTALNG (in
 isoform BMP1-5).
 /FtId=VSP_005465.
 Missing (in isoform BMP1-5).
 /FtId=VSP_005466.
 DDECKSKNGGCGQD -> GGELFGILGHPRRP (in
 isoform BMP1-6).


```

FT  /FTid=VSP_005467.
FT  Missing (in isoform BMP1-6).
FT  /FTid=VSP_005468.
FT  VARSPLIC 718 986
FT  VARSPLIC 703 823
FT  DKECDKSDNGCCODCCVNTFSYSCQCRSGFVLDNRDCK
FT  EAGCDHKTSTSTGTTISPMWPKTSPSKCECTWALSIFGR
FT  VKLTFMEWDIESQPCADYDLFVDPGRAPVGRG
FT  -> VLEGAGDRSHSLGIELLCPLALDTPAPPSALHGD
FT  THAHTHTGHTHCPHAGETGCPPLASRLSPGSGHLLTA
FT  POGESYLDPMTHRGDPKRRRRRSKTFSLTPATPFGIWA
FT  L (in isoform BMP1-7).
FT  /FTid=VSP_005469.
FT  VARSPLIC 824 986
FT  Missing (in isoform BMP1-7).
FT  /FTid=VSP_005470.
FT  CONFLICT 748 748
FT  CONFLICT 934 934
FT  R -> N (IN REF. 4).
FT  R -> S (IN REF. 4).
SQ  SEQUENCE 986 AA; 111248 MW; F89201913AC3CBB4 CRC64;

Query Match 9.1%; Score 169; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NGSHSRPFHTYPRNTVLVWRLVA--VEENVWILTFDERFGLEDPEDDICKDFVEVEE 113
Db 599 NGSTISDGPWEKPEYPPNKNCTMQLVAPTOYRISLQDFEETEG-----NDVCKYDFVEYRS 653

Qy 114 --PSDGTILGRMGSGTVPGKQISGNQIRIFVSDSEFPSEPCITHY 160
Db 654 GLTADSKLHGKFCDS-EKPEVITSQYNNRVKFSNDNTV-SKKGPKAHF 700

RESULT 5
BMP1_MOUSE
ID _BMP1_MOUSE STANDARD; PRT; 991 AA.
AC P98063;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tollold protein) (mtld).
GN BMP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=94229342; PubMed=8174772;
RA Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT which is related to the Drosophila dorsoventral gene tollold and
RT encodes a putative astacin metalloendopeptidase."
RL Dev. Biol. 163:175-183(1994).
CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC and III. Induces cartilage and bone formation.
CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type
CC III.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-
CC endopeptidase enhancer protein.
CC -1- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC and floor plate region of the neural tube. Less in developing
CC membranes and endochondral bone, submucosa of intestine, dermis
CC of skin and the mesenchyme of spleen and lung.
CC -1- SIMILARITY: Belongs to peptidase family M12A.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 5 CUB domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ch/announce/
CC or send an email to license@ebi.ebi.ch).
CC -----
CC EMBL; L24755; AAA37306.1; -.
CC PIR; I49540; I49540.
CC HSSP; P00736; IAPQ.
CC MEROPS; M12.005; -.
CC MGD; MGI:88176; Bmp1.
DR InterPro; IPR000153; Asx_hydroxyl_5.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006025; peptidase_M.
DR InterPro; IPR001506; peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
KW Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein; Zymogen.
FT SIGNAL 1 25
FT PROPEP 26 125
FT CHAIN 126 991
FT DOMAIN 126 326
FT DOMAIN 327 439
FT DOMAIN 440 551
FT DOMAIN 552 593
FT DOMAIN 596 707
FT DOMAIN 708 748
FT DOMAIN 752 864
FT DOMAIN 865 981
FT METAL 218 218
FT ACT_SITE 219 219
FT METAL 222 222
FT METAL 228 228
FT DISULFID 188 191
FT DISULFID 327 353
FT DISULFID 380 402
FT DISULFID 440 466
FT DISULFID 493 515
FT DISULFID 556 568
FT DISULFID 564 577
FT DISULFID 579 592
FT DISULFID 596 622
FT DISULFID 649 671
FT DISULFID 712 723
FT DISULFID 719 732
FT DISULFID 734 747
FT CARBOHYD 96 96
FT CARBOHYD 147 147
FT CARBOHYD 337 337
FT CARBOHYD 368 368
FT CARBOHYD 604 604
SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;

Query Match 9.1%; Score 169; DB 1; Length 991;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NGSHSRPFHTYPRNTVLVWRLVA--VEENVWILTFDERFGLEDPEDDICKDFVEVEE 113

```

```

Db      604  NGSITLPGMPKPEYPPNKNCKIOWGLVAPTOYRISLQDFDFETEG-----NDVCKYDVEVRS 658
Oy      114  --PSSGTLGRWCQSGGYTPGKQISKGNQIRIRFVDETFPSPEGCIFY 160
Db      659  GLTADSKLHGKFCGS-EKPEVITSSQYNNMRVFKSDNTV-SKKGKRAHF 705

RESULT 6
NRP2_HUMAN
ID      NRP2_HUMAN      STANDARD;      PRT;      931 AA.
AC      O60462; O14820; O14821;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neupophilin-2 precursor (Vascular endothelial cell growth factor 165
DE      receptor 2).
NRP2 OR VEGF165R2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
MEDLINE=97470889; PubMed=9331348;
RA      Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT      "Neupophilin-2, a novel member of the neupophilin family, is a high
RT      affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT      III."
RL      Neuron 19:547-559(1997).
[2]
SEQUENCE FROM N.A. (ISOFORM A22).
RC      TISSUE=Breast;
RX      MEDLINE=98188099; PubMed=9529250;
RA      Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.;
RT      "Neupophilin-1 is expressed by endothelial and tumor cells as an
RT      isoform-specific receptor for vascular endothelial growth factor.";
RL      Cell 92:735-745(1998).
[3]
CHARACTERIZATION.
RP      MEDLINE=20309748; PubMed=10748121;
RA      Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT      "Neupophilin-2 and neupophilin-1 are receptors for the 165-amino acid
RT      form of vascular endothelial growth factor (VEGF) and of placenta
RT      growth factor-2, but only neupophilin-2 functions as a receptor for
RT      the 145-amino acid form of VEGF."
RL      J. Biol. Chem. 275:18040-18045(2000).
CC      -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
CC      and VEGF-145 isoforms of VEGF, and the PlGF-2 isoform of PGF.
CC      -1- SUBUNIT: Neupophilin-2 probably forms a heteromeric complex with
CC      neupophilin-1 in order to be a functional semaphorin 3C receptor.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=A22;
CC      IsoId=O60462-1; Sequence=Displayed;
CC      Name=A0;
CC      IsoId=O60462-2; Sequence=VSP_004342;
CC      Name=A17;
CC      IsoId=O60462-3; Sequence=VSP_004341;
CC      -1- SIMILARITY: Belongs to the neupophilin family.
CC      -1- SIMILARITY: Contains 2 CUB domains.
CC      -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC      -1- SIMILARITY: Contains 1 MAM domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/commence/
CC      or send an email to license@isb-sib.ch).

```

DR EMBL; AF022859; AAC51788.1; -
DR EMBL; AF022860; AAC51789.1; -
DR EMBL; AF016098; AAC12922.1; -
DR HSSB; F12259; ICZT.
DR Genew; HGNC:8005; NRP2.
DR MIM; 602070; -
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0005021; F:vacular endothelial growth factor receptor..; TAS.
DR GO; GO:0007411; P:axon guidance; TAS.
DR InterPro; IPR00859; CUB.
DR InterPro; IPR00421; FA58_C.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR00998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_P8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00042; MAMDMAIN.
DR SMART; SMO0042; CUB; 2.
DR SMART; SMO0231; FA58C; 2.
DR SMART; SMO0137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neurexine; Signal; Repeat; Receptor;
KX Alternative splicing.
FT SIGNAL 1 20 OR 22 (POTENTIAL).
FT CHAIN 21 931 NEUROPLIN-2.
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 865 889 POTENTIAL.
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/F8 TYPE C 1.
FT DOMAIN 434 592 F5/F8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DOMAIN 671 674 POLY-SER.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 839 839 N-LINKED (GLCNAC...) (POTENTIAL).
FT VASPLIC 809 813 Missing (in isoform A17).
FT VASPLIC 809 813 /FTid=VSP 004341.
FT VASPLIC 809 830 Missing (in isoform A0).
FT CONFLICT 602 602 E -> K (IN REF. 1).
FT SEQUENCE 931 AA; 104830 MW; 270CGAEE69A0A797C CRC64;
Query Match 8.9%; Score 164.5; DB 1; Length 931;
Best Local Similarity 29.9%; Pred. No. 4.2e-06;
Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5
Qy 1 MSLEGLLVTSALAGRGRTQAESLSLKPFSSNKKEONGVDPPGHERIIITSTNGSIHS 60
Db 1 MDMPPLTWFL-----YFSHQVRGGDDPPCGGRLSKNDAAYITS 42
Qy 61 RPFPHTYPRNTVLVWRVAVENWMIQLTPDERFGLEDPEDDICKYDFVEVE--EPSDET 118
Db 43 PGYQDPDSHQNCEMVIYAAPRNCKIVLFNPHPFEIKHD--CKYDFEIRDGSAD 99
Qy 119 ILGWCCSGGVPGKQISKGNDIRIRFVSDEFFPSRPGCIKHNI 162
Db 100 LLAGRCGN-IAPPTIISGSMLYIKFTSD-YAROGAGPSLRYEI 141

```

RESULT 7
NRPL_RAT ID NRPL_RAT STANDARD: PRT: 922 AA.
AC Q9QW09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
GN NRPL.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kojodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neuropilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -1- FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsant activity of semaphorins. It binds to semaphorin 3A, the PLGF-2 isoform of RGF, the VEGF-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis. It may regulate VEGF-induced angiogenesis (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Found in the embryonic nervous system.
CC -1- SIMILARITY: Belongs to the neuropilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF016296; AAC53337.1; -.
DR HSSP; P12259; ICZT.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR008979; Gal_Bind_Like.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PRO0020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01285; FAS8C_1; 2.
DR PROSITE; PS01286; FAS8C_2; 2.
DR PROSITE; PS0022; FAS8C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS0060; MAM_2; 1.
DR Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
KM
FT SIGNAL 1 21
FT CHAIN 22 922
FT DOMAIN 22 855
FT TRANSMEM 856 880
FT DOMAIN 881 922
FT DOMAIN 27 141
FT DOMAIN 147 265

```

```

FT DOMAIN 275 424
FT DOMAIN 431 583
FT DOMAIN 645 811
FT DISULFID 27 54
FT DISULFID 82 104
FT DISULFID 147 173
FT DISULFID 206 228
FT DISULFID 275 424
FT DISULFID 431 583
FT CARBOHYD 150 150
FT CARBOHYD 261 261
FT CARBOHYD 300 300
FT CARBOHYD 522 522
FT CARBOHYD 841 841
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD09B0F2E CRC64;

Query Match 8.8%; Score 163.5; DB 1; Length 922;
Best Local Similarity 36.5%; Pred. No. 5.1e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

QY 50 ITVSTNGSIHSPRPHTYPRNTLVWRLVAEENWVITQTFDERPGLDEPDDICTKDFV 109
DB 31 IKIENPGYLSPPGYPHSYSEKCEWLIQAEPEYQIRIMINFPHFLEDRD---CKYDYV 87
QY 110 EV--EESPDDGTLGRMCGSGTVPGKQISKQNIIRFPDSDEYFSEBGFCHYNI 162
DB 88 EVIDENEGKRLMGKFCCK-IAPSPVSSGFFLFKIFVSD-YETHGAGFSIRYEI 140

RESULT 8
NRPL_RAT ID NRPL_RAT STANDARD: PRT: 925 AA.
AC Q35276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NRPL2.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kojodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neuropilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165 and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of RGF.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Found in certain neuronal populations of the CNS and in other nonneuronal tissues including mesenchymal tissue lining in the ribs.
CC -1- SIMILARITY: Belongs to the neuropilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF016297; AAC53338.1; -.
DR HSSP; P12259; ICZT.
DR InterPro; IPR000859; CUB.

```

DR InterPro; IPR000421; FASB_C.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FASB_C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01285; FASB_C; 2.
 DR PROSITE; PS01285; FASB_C; 2.
 DR PROSITE; PS01286; FASB_C; 2.
 DR PROSITE; PS50022; FASB_C; 2.
 DR PROSITE; PS50060; MAM; 2; 1.
 DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
 FT SIGMIL 1 22
 FT CHAIN 23 925
 FT DOMAIN 23 858
 FT TRANSMEM 859 883
 FT DOMAIN 884 925
 FT DOMAIN 28 142
 FT DOMAIN 149 267
 FT DOMAIN 277 427
 FT DOMAIN 434 592
 FT DOMAIN 642 802
 FT DISULFID 28 55
 FT DISULFID 83 105
 FT DISULFID 149 175
 FT DISULFID 208 230
 FT DISULFID 277 427
 FT CARBOHYD 152 152
 FT CARBOHYD 157 157
 FT CARBOHYD 629 629
 FT CARBOHYD 833 833
 FT CARBOHYD 834 834
 SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CRC64;

Query Match 8.8%; Score 163; DB 1; Length 925;
 Best Local Similarity 33.8%; Pred. No. 5.6e-06;
 Matches 45; Conservative 20; Mismatches 60; Indels 8; Gaps 5;

QY 32 PSSNKGQNGVQDQHERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTPD 91
 DB 15 FSGHAKYRS-QQDPCCGRLNSKQAGYITSPGYQDPVSHQNCMVVYAPENQKIVLNF 73
 QY 92 ERFGLDEPDDICKYDFVEVE--EPDGLTLGRWCGSGVYVGRKQISKGNQIRIRFVSDEY 149
 DB 74 PHEIEIKHD---CKYDFIEIRDDSDSADLGRHCGN-IAPPTLISSGSLYIKFTSD-Y 128
 QY 150 FPEPFGCIHYN 162
 DB 129 ARQAGAFSLRYEI 141

RESULT 9
 VEGD RAT
 ID VEGD RAT STANDARD; PRT; 326 AA.
 AC 0352E1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
 GN FIGF OR VEGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;

RA Yamada Y., Hirata Y., Nezu J., Shimane M.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor (By similarity).
 CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).
 CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF014827; AAB6557.1; -.
 DR HSSP; P15692; 1VPP.
 DR InterPro; IPR004153; CXKCX repeat.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; PF03128; CXKCX; 1.
 DR Pfam; PF00341; PDGF; 1.
 DR ProDom; PD001629; PD_growth_factor; 1.
 DR SMART; SM00441; PDGF; 1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS00278; PDGF_2; 1.
 DR Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; cleavage on pair of basic residues; Multigene family.
 KM
 FT SIGMIL 1 21
 FT PROPEP 22 93
 FT CHAIN 94 210
 FT PROPEP 211 326
 FT DOMAIN 227 317
 FT REPEAT 227 242
 FT REPEAT 263 278
 FT REPEAT 282 298
 FT REPEAT 306 317
 FT DISULFID 116 158
 FT DISULFID 147 194
 FT DISULFID 151 196
 FT DISULFID 141 141
 FT DISULFID 150 150
 FT CARBOHYD 160 160
 FT CARBOHYD 190 190
 FT CARBOHYD 292 292
 SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

Query Match 8.7%; Score 162.5; DB 1; Length 326;
 Best Local Similarity 30.0%; Pred. No. 1.6e-06;
 Matches 61; Conservative 23; Mismatches 80; Indels 39; Gaps 9;

QY 155 GSCIHNIYMPQTEVSSVPPSLPDLNNAITASTEDLIRYEPERMQLDED 214
 DB 21 GSIEHRAVKDVLSRSSRSLERS-----EQGIKASTLEILLQVHSSDWK----- 68
 QY 215 IYRPTWOLGKAFVGRKSR-----VVDNLTEVRRLYSCTPRNFSVIRRE 262
 DB 69 IWRCRKLKSLANDVSRSTSHSTRFAFYDTETLKVIDEMQRQCSPRECVASR 128
 QY 263 L-KRTDTIFWPGCLLVKRCGNCACCLHNCNCCQCV--PSKYTKYHVEVLQLRPTGYR 318

Db 129 LGTTNTEFKPCVNVFRCG---CC--NEESVMCMNTSTYSIKQLEISV--PLTSV- 180

Qy 319 GLHKSJVDVALEHHECCVCG 341

Db 181 ---BELVAVKIANHGTCKCLPTG 200

RESULT 10

NRPI_MOUSE STANDARD; PRT; 923 AA.

AC P97333;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuropilin-1 precursor (A5 protein).

GN NRPI OR NRP.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c; TISSUE=Embryonic brain;

RX MEDLINE=96353149; PubMed=8748368;

RA Kawakami A., Kiteaukawa T., Takagi S., Fujisawa H.;

RT "Developmentally regulated expression of a cell surface protein, neuropilin, in the mouse nervous system.";

RL J. Neurobiol. 29:1-17(1996).

CC -1- FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsive activity of semaphorins. It binds to semaphorin 3A, the PLGF-2 isoform of PGF, the VEGF-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis. It may regulate VEGF-induced angiogenesis (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: Nervous system.

CC -1- SIMILARITY: Belongs to the neuropilin family.

CC -1- SIMILARITY: Contains 2 CUB domains.

CC -1- SIMILARITY: Contains 2 P5/8 type C domains.

CC -1- SIMILARITY: Contains 1 MAM domain.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements) or send an email to license@ebi.ac.uk).

CC -----

DR EMBL; D50086; BAA08789.1; -.

DR HSSP; P12259; 1CZT.

DR MGD; MGI:106206; NRP.

DR GO; GO:0017154; F:semaphorin receptor activity; IGI.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR000421; P58 C.

DR InterPro; IPR008979; Gal_bind_like.

DR InterPro; IPR000998; MAM_domain.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00754; P5_P8_type_C; 2.

DR Pfam; PF00629; MAM; 1.

DR PRINTS; PRO0020; MAMDOMAIN.

DR SMART; SM00042; CUB; 2.

DR SMART; SM00231; P58C; 2.

DR SMART; SM00137; P58C; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; P58C; 1.

DR PROSITE; PS01286; P58C; 2.

DR PROSITE; PS00022; P58C; 3.

DR PROSITE; PS00740; MAM_1; 1.

DR PROSITE; PS50060; MAM_2; 1.

KW Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;

KW Receptor.

FT SIGNAL 1 21

FT CHAIN 22 923

FT DOMAIN 22 856

FT TRANSMEM 857 879

FT DOMAIN 880 923

FT DOMAIN 27 141

FT DOMAIN 147 265

FT DOMAIN 275 424

FT DOMAIN 431 583

FT DOMAIN 645 811

FT DISULFID 82 54

FT DISULFID 27 104

FT DISULFID 147 173

FT DISULFID 206 228

FT DISULFID 275 424

FT DISULFID 431 583

FT CARBOHYD 150 150

FT CARBOHYD 261 261

FT CARBOHYD 300 300

FT CARBOHYD 522 522

FT CARBOHYD 842 842

SO SEQUENCE 923 AA; 103020 MW; 0644B8A170796808 CRC64;

Query Match 8.6%; Score 160.5; DB 1; Length 923;

Best Local Similarity 36.5%; Pred. No. 9.2e-06;

Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

Qy 50 ITVSTNGSIHSPPHPTYPRTVTLVRLVAEENWVLTQTFDERFGLDEPDIDCKYDFV 109

Db 31 IKINPGVLISPGVPHSHPEKCEMILQAPVQRILINNHFDLEDRD---CKDYV 87

Qy 110 EV--EPPSDGTLIRMGCGSGTVPGKQISKNGQIRVSDRYPPSPGFCIHVI 162

Db 88 EVIDENEGRLMGKFCGK-IAPSPVWSGPFILIKRVSD-YETHGAGFSIRYEI 140

RESULT 11

NRP2_MOUSE STANDARD; PRT; 931 AA.

ID_NRP2_MOUSE

AC Q35375; Q35373; Q35374; Q35376; Q35377; Q35378;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).

GN NRP2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

[1]

RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).

RC STRAIN=BALB/c;

RX MEDLINE=97470888; PubMed=9333348;

RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;

RT "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III."

RL Neuron 19:547-559(1997).

CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165 and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of PGF.

CC -1- SUBUNIT: Neuropilin-2 probably forms a heteromeric complex with neuropilin-1 in order to be a functional semaphorin E receptor.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=6;

CC Name=A22;

CC IsoId=O35375-1; Sequence=Displayed;

CC Name=A0;

CC IsoId=O35375-2; Sequence=VSP_004344;

CC Name=A5;

CC IsoId=O35375-3; Sequence=VSP_004345;

FT	DISULFID	765	778	BY SIMILARITY.
FT <td>DISULFID</td> <td>783</td> <td>809</td> <td>BY SIMILARITY.</td>	DISULFID	783	809	BY SIMILARITY.
FT <td>DISULFID</td> <td>836</td> <td>858</td> <td>BY SIMILARITY.</td>	DISULFID	836	858	BY SIMILARITY.
FT <td>DISULFID</td> <td>896</td> <td>926</td> <td>BY SIMILARITY.</td>	DISULFID	896	926	BY SIMILARITY.
FT <td>DISULFID</td> <td>953</td> <td>975</td> <td>BY SIMILARITY.</td>	DISULFID	953	975	BY SIMILARITY.
FT <td>CARBOHYD</td> <td>129</td> <td>129</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	129	129	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>178</td> <td>178</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	178	178	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>368</td> <td>368</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	368	368	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>399</td> <td>399</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	399	399	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>635</td> <td>635</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	635	635	N-LINKED (GLCNAC. . .)
SO <td>SEQUENCE</td> <td>1022 AA;</td> <td>115536 MW;</td> <td>A68CA1D0E41793F9 CRC64;</td>	SEQUENCE	1022 AA;	115536 MW;	A68CA1D0E41793F9 CRC64;
Query Match				
Query	Similarity	8.6%;	Score 159;	DB 1; Length 1022;
Match	Local	Similarity 39.8%;	Pred. No. 1.4e-05;	
		Conservative 43;	Mismatches 19;	Indels 8; Gaps 6;
Db	NGSIHSPRPFTPTVRLVRLVAENVNVIQTPDERFGLDEPDICRYDFVEYEB-	113		
	635 NGITITTPMPPEYVPPNKCWQVAPQ-VKISQF-EAFPLEG--NEVCKYDYVVRSG	690		
Qy	114 -PSDGTILGRMCGSGTVPGKQISKNGQIRIRFVSDXEPSPGFCIH	160		
Db	691 LSSDSKLHGKYGCT-EVPEVITTSQYNNRIEFKSDNTV-SKGGKAPF	736		
RESULT 13				
NRPI_HUMAN	STANDARD;	PRT;	923 AA.	
ID	_NRPI_HUMAN			
AC	014786; 060461;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).			
GN	NRPI OR NRP OR VEGF165R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=97433084; PubMed=9288753;			
RA	He Z., Teeslar-Lavigne M.;			
RT	"Neuropilin-1 is a receptor for the axonal chemorepellent semaphorin III.";			
RL	Cell 90:739-751(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.			
RC	TISSUE=Breast;			
RX	MEDLINE=96188099; PubMed=9529250;			
RA	Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;			
RT	"Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";			
RL	Cell 92:735-745(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.			
RC	TISSUE=Prostatic adenocarcinoma;			
RX	MEDLINE=20183929; PubMed=10688890;			
RA	Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S.,			
RA	Soker S., Klagsbrun M.;			
RT	"Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=20309748; PubMed=10748121;			
RA	Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;			
RT	"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";			
RL	J. Biol. Chem. 275:18040-18045(2000).			

CC -1- FUNCTION: The membrane-bound isoform 1 is a receptor involved in
 CC the development of the cardiovascular system, in angiogenesis, in
 CC the formation of certain neuronal circuits and in organogenesis
 CC outside the nervous system. It mediates the chemorepulsive
 CC activity of semaphorins. It binds to semaphorin 3A, the p16G-2
 CC isoform of p16G. The VEGF-165 isoform of VEGF and VEGF-B.
 CC Coexpression with KDR results in increased VEGF-165 binding to KDR
 CC as well as increased chemotaxis. It may regulate VEGF-induced
 CC angiogenesis.
 CC -1- FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to
 CC inhibit its binding to cells. It may also induce apoptosis by
 CC sequestering VEGF-165. May bind as well various members of the
 CC semaphorin family. Its expression has an adverse effect on blood
 CC vessel number and integrity.
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein. Isoform 2 is
 CC secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Membrane-bound;
 CC IsoId=O14786-1; Sequence=Displayed;
 CC Name=2; Synonyms=Soluble, SNRP1;
 CC IsoId=O14786-2; Sequence=VSP_004339, VSP_004340;
 CC -1- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not
 CC seem to overlap. Isoform 1 is expressed by the blood vessels of
 CC different tissues. In the developing embryo it is found
 CC predominantly in the nervous system. In adult tissues, it is
 CC highly expressed in heart and placenta; moderately in lung, liver,
 CC skeletal muscle, kidney and pancreas; and low in adult brain.
 CC Isoform 2 is found in liver hepatocytes, kidney distal and
 CC proximal tubules.
 CC -1- SIMILARITY: Belongs to the neuropilin family.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: Contains 1 MAM domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF018956; AAC51759.1; -;
 CC EMBL; AF016050; AAC12921.1; -;
 CC EMBL; AF145712; AAF44344.1; -;
 CC PDB; 1KEX; 28-JAN-03
 CC Genew; HGNC; 8004; NRPL.
 CC MIM; 602069; -;
 CC DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.
 CC DR GO; GO:0007411; P:axon guidance; TAS.
 CC DR GO; GO:0007267; P:cell-cell signaling; TAS.
 CC DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
 CC DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
 CC DR InterPro; IPR000859; CUB.
 CC DR InterPro; IPR000421; FAS8_C.
 CC DR InterPro; IPR008979; Gal_Bind_Like.
 CC DR InterPro; IPR000998; MAM_domain.
 CC Pfam; PF00431; CUB; 2.
 CC Pfam; PF00754; F5_F8_Type_C; 2.
 CC Pfam; PF00629; MAM; 1.
 CC PRINTS; PR00020; MAMDOMAIN.
 CC SMART; SM00042; CUB; 2.
 CC SMART; SM00231; FAS8C; 2.
 CC SMART; SM00137; MAM; 1.
 CC PROSITE; PS01180; CUB; 2.
 CC PROSITE; PS01285; FAS8C_1; 2.
 CC PROSITE; PS01286; FAS8C_2; 2.
 CC PROSITE; PS50022; FAS8C_3; 2.
 CC PROSITE; PS00740; MAM_1; 1.
 CC PROSITE; PS50060; MAM_2; 1.
 CC Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;

KW Receptor; Alternative splicing; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 923
 FT DOMAIN 22 856
 FT TRANSMEM 857 879
 FT DOMAIN 880 923
 FT DOMAIN 27 141
 FT DOMAIN 147 265
 FT DOMAIN 275 424
 FT DOMAIN 431 583
 FT DOMAIN 645 811
 FT DISULFID 27 54
 FT DISULFID 82 104
 FT DISULFID 147 173
 FT DISULFID 206 228
 FT DISULFID 275 424
 FT DISULFID 431 583
 FT CARBOHYD 150 150
 FT CARBOHYD 261 261
 FT CARBOHYD 300 300
 FT CARBOHYD 522 522
 FT CARBOHYD 842 842
 FT VARSPPLIC 642 644
 FT VARSPPLIC 645 923
 FT CONFLICT 26 26
 FT CONFLICT 749 749
 FT CONFLICT 855 855
 FT SEQUENCE 923 AA; 103120 MW; ADKADCA48495D57 CRC64;
 Query Match 8.5%; Score 158.5; DB 1; Length 923;
 Best Local Similarity 35.7%; Pred. No. 1.4e-05;
 Matches 41; Conservative 18; Mismatches 49; Indels 7; Gaps 4;
 QY 50 IVYSTNGSIHSPPFTTTRNTVLRVLAIVENWITQTFPBRFLEDPEDICKYDV 109
 DB 31 IKIESGYLTSGYPSHYSRSEKCELTQAPPYQRIIMNFMHPLEDRD--CKYDV 87
 QY 110 EV--EESPDDTLGRWCGSGTVPGKQISKNGQIRIRFVSDVDEYPPSPGCIHNI 162
 DB 88 EYFDGENENHGRKCGK-TAPPVSSGPFLFIKVS-D-YETHGAGFSIRYEI 140
 RESULT 14
 NRPL_CHICK STANDARD; PRT; 914 AA.
 AC P79795;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 GN Neuropilin-1 precursor (AS protein).
 OS NRPL OR NRP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Embryonic brain;
 RX MEDLINE=95324761; PubMed=7601310;
 RA Takagi S., Kasuya Y., Shimizu M., Matsunura T., Tsuboi M., Kawakami A.,
 RA Fujisawa H.;
 RT "Expression of a cell adhesion molecule, neuropilin, in the
 RT developing chick nervous system.";
 RL Dev. Biol. 170:207-222 (1995).
 CC -1- FUNCTION: Receptor involved in the development of the
 CC cardiovascular system, in angiogenesis, in the formation of
 CC certain neuronal circuits and in organogenesis outside the nervous
 CC system. It mediates the chemorepulsive activity of semaphorins (By
 CC similarity). Seems to have calcium-independent cell adhesion
 CC properties.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Developing nervous system; optic tectum
 CC (layers D and E of SGRS), amacrine cells of retina, neurites of
 CC dorsal root ganglia. Also expressed in nonneuronal cells, e.g.
 CC blood vessels in the entire embryo.
 CC -1- SIMILARITY: Belongs to the neuropilin family.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: Contains 1 MAM domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by, and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D45416; BAA08256.1; -
 DR HSSP: P12259; IC2T
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000421; FAS8_C.
 DR InterPro: IPR008979; Gal Bind like.
 DR InterPro: IPR000998; MAM_domain.
 DR Pfam: PF00431; CUB; 2.
 DR Pfam: PF00754; F5_F8_type_C; 2.
 DR Pfam: PF00629; MAM; 1.
 DR PRINTS: PR00020; MAMDOMAIN.
 DR SMART: SM00042; CUB; 2.
 DR SMART: SM00231; FAS8C; 2.
 DR SMART: SM00137; MAM; 1.
 DR PROSITE: PS01180; CUB; 2.
 DR PROSITE: PS01285; FAS8C_1; 2.
 DR PROSITE: PS01286; FAS8C_2; 2.
 DR PROSITE: PS50022; FAS8C_3; 2.
 DR PROSITE: PS00740; MAM_1; 1.
 DR PROSITE: PS50060; MAM_2; 1.
 DR Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;
 KM Receptor; Cell adhesion.
 FT SIGNAL 18
 FT CHAIN 19 914
 FT DOMAIN 20 847
 FT TRANSMEM 848 870
 FT DOMAIN 871 914
 FT DOMAIN 25 139
 FT DOMAIN 145 263
 FT DOMAIN 429 581
 FT DOMAIN 636 801
 FT DISULFID 25 52
 FT DISULFID 80 102
 FT DISULFID 145 171
 FT DISULFID 204 226
 FT DISULFID 273 422
 FT DISULFID 429 581
 SQ SEQUENCE 914 AA; 102480 MW; DD2EE6DFCBB68C CRC64;

Query Match 8.4%; Score 157; DB 1; Length 914;
 Best Local Similarity 29.4%; Pred. No. 1.8e-05;
 Matches 52; Conservative 27; Mismatches 68; Indels 30; Gaps 9;

QY 50 ITVSTNSIHSRPHRYPRNTVYVRLVAVENWVQLTFDERFGLEDDEDDICRKYDV 109
 DB 29 IKLUSPYLTSFGYPSQYHSQKCEWLIQAEPYQRTMINPFDLEDRD--CKYDV 85
 QY 110 EV--EBSDDGTLIRMGSGTVPKQISKNQIRIRFVSDYFSPSEGCFTYNIWV--P 165
 DB 86 EVIDGDNAEGRIMWKYCGK-IAPPLVLSGPGYLFIKTVSD-YETHGAGFSIRYVFRGCP 143
 QY 166 Q----PTEAVSPSLP--PSALPLDL-----LNNAITAFSTEDLIRLYEPE 206
 DB 144 ECSNHFSSSGMIKSPGFPEKYPMNSLECTYIIAPKMSSEILFESEFE-----LEPD 195

RESULT 15
 ID PCOL_HUMAN STANDARD; PRT; 449 AA.
 AC Q05113; O14550;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
 DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-
 DE proteinase enhancer protein).
 GN Homo sapiens (Human)
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=95014462; PubMed=7523404;
 RA Takahara K., Kessler E., Biniaminov L., Brusel M., Bddy R.L.,
 RA Tani-Sait S., Shows T.B., Greenspan D.S.;
 RT "Type I procollagen COOH-terminal proteinase enhancer protein:
 RT identification, primary structure, and chromosomal localization of the
 RT cognate human gene (PCOLCE).";
 RL J Biol. Chem. 269:26280-26285 (1994).
 RN REVIEWS TO 56; 154 AND 373.
 RA Kessler E.;
 RL Unpublished observations (FEB-2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,
 RA Morisaki N., Saito Y.;
 RT "Smooth muscle cell derived procollagen C-protease enhancer protein";
 RL Cell Struct. Funct. 21:662-662 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99018118; PubMed=9799793;
 RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
 RA Tsui L.-C., Rosenthal A.;
 RT "Large-scale sequencing of two regions in human chromosome 7q22:
 RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
 RT reveals 17 genes.";
 RL Genome Res. 8:1060-1073 (1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99134301; PubMed=9933570;
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
 RT "Structural organization and expression patterns of the human and
 RT mouse genes for the type I procollagen COOH-terminal proteinase
 RT enhancer protein";
 RL Genomics 55:229-234 (1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Vallier J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
 RX MEDLINE=20092917; PubMed=10625689;
 RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
 RA Banda M.J.;
 RT "Post-translational proteolytic processing of procollagen C-terminal
 RT proteinase enhancer releases a metalloproteinase inhibitor.";
 RL J. Biol. Chem. 275:1384-1390(2000).
 CC -|- FUNCTION: Binds to the COOH-terminal propeptide of type I
 CC procollagen and enhances procollagen C-proteinase activity.
 CC -|- FUNCTION: C-terminal processed part of PCPE (CT-PCPE) may have an
 CC metalloproteinase inhibitory activity.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- PTM: C-terminally processed at multiple positions.
 CC -|- SIMILARITY: Contains 2 CUB domains.
 CC -|- SIMILARITY: Contains 1 NTR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L33799; AAA61949.1; ALT_SEQ.
 DR EMBL; AB008549; BAA23281.1; -;
 DR EMBL; AF053356; AAC78800.1; -;
 DR EMBL; AF083655; AAD16041.1; -;
 DR EMBL; BC000574; AAH00574.1; -;
 DR EMBL; BC033205; AAH33205.1; -;
 DR GeneW; HGNC:8738; PCOLCE.
 DR MIM; 600270; -;
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF00451; CUB; 2.
 DR Pfam; PF01759; NTR; 1.
 DR SMART; SM00643; C345C; 1.
 DR SMART; SM00042; CUB; 2.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS50189; NTR; 1.
 DR KW Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 449 PROCOLLAGEN C-PROTEINASE ENHANCER
 FT PROTEIN.
 FT DOMAIN 37 149 CUB 1.
 FT DOMAIN 159 273 CUB 2.
 FT DOMAIN 318 437 NTR.
 FT SITE 287 288 CLEAVAGE.
 FT SITE 288 289 CLEAVAGE.
 FT SITE 293 294 CLEAVAGE.
 FT SITE 299 300 CLEAVAGE.
 FT SITE 303 304 CLEAVAGE.
 FT CARBOHYD 29 29 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC..) (POTENTIAL).
 SQ SEQUENCE 449 AA; 47972 MW; 3D86430158648796 CRC64;

Query Match 8.3%; Score 154; DB 1; Length 449;
 Best Local Similarity 33.8%; Pred. No. 1.3e-05;

Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;

QY 56 GSIIHSPFPH-YPRTVLVRLVAVENWVQLTFDERGLEDPEDDICKYDFVEV---111
 Db 168 GTLTENWESDYPPGIGSCSWHIIAPPDV-IALTF-EKFDLE--PTYCRIDSVSVENG 223

QY 112 EEPDGTIIGRWCGSGTVPQKQISKNGQIRIRFVSDVEYFPEFGCIHYNIWPOFT---168
 Db 224 AVSDDRRLRGKFGCD-AVPGSISSEGNELVQFVSDLSVTAD-GFSASYK-TLPGTAXE 280
 QY 169 -----EAVSPSV-LPPSALP 182
 Db 281 GGGPGRKGTETPRVKLPPKSP 302

Search completed: May 27, 2004, 15:45:16
 Job time : 12.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:21 ; Search time 36.5 Seconds

(without alignments)
2982.295 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858
Sequence: 1 MSLEGLLVTSALAGQRGR.....DVALHHEDCYCRSGTG 345

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL.25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rv1rus:*
17: sp_bacteriopl:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	4	Q9NRA1
2	1851	99.6	345	4	Q9UL22
3	1664	89.6	345	11	Q9OY71
4	1662	89.5	345	11	Q8C119
5	1646	88.6	345	11	Q9EOX6
6	1635	88.0	345	11	Q9JHV8
7	1614	86.9	345	13	Q91946
8	1260	67.8	258	11	Q8K429
9	741.5	39.9	370	4	Q9GZP0
10	740.5	39.9	364	4	Q9BWV5
11	737.5	39.7	370	11	Q9ZS17
12	736	39.6	370	11	Q9EGT1
13	435.5	23.4	261	11	Q8K2L3
14	190.5	10.3	923	13	Q8QFX6
15	190.5	10.3	923	13	Q8AXP1
16	183	9.8	3623	4	Q60494

17	182	9.8	691	13	O57658
18	180	9.7	34	11	O99JM4
19	176	9.5	977	13	O91925
20	176	9.5	3623	11	O70244
21	172	9.3	1012	11	O9WVM6
22	171	9.2	735	13	O57381
23	171	9.2	926	4	O9U000
24	171	9.2	1015	4	O9Y617
25	169	9.1	241	11	O9Z135
26	165.5	8.9	145	11	O8BP20
27	165.5	8.9	926	11	O8Q2Y7
28	164.5	8.9	555	4	O9H2E2
29	164.5	8.9	901	4	O9H2E4
30	164.5	8.9	901	4	O9H2D5
31	164.5	8.9	906	4	O9H2D4
32	164.5	8.9	906	4	O9H2E3
33	163.5	8.8	921	11	O9QX38
34	163.5	8.8	3620	6	O9TU53
35	161.5	8.7	1007	13	O8J128
36	160	8.6	413	13	O7SV25
37	159.5	8.6	931	4	O7Z3T9
38	158.5	8.5	609	4	O96190
39	158.5	8.5	644	4	O961H5
40	158.5	8.5	704	4	O9H2E1
41	158.5	8.5	923	4	O86T59
42	157.5	8.5	905	13	O80014
43	157.5	8.5	919	13	O8UVR0
44	157.5	8.5	936	13	O8UVQ9
45	157	8.4	1008	13	O9DER7

ALIGNMENTS

RESULT 1

Q9NRA1 PRELIMINARY; PRT; 345 AA.

ID Q9NRA1

AC Q9NRA1; 01-OCT-2000 (TREMUR1.15, Created)

DT 01-OCT-2000 (TREMUR1.15, Last sequence update)

DT 01-OCT-2003 (TREMUR1.25, Last annotation update)

DE Platelet-derived growth factor C.

OS Homo sapiens (Human).

OC Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

OX [1]

RP TISSUE=Lung;

RP SEQUENCE FROM N.A.

RC MERLIN=20266201; Pubmed=10806482;

RX Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uteja M., Backstrom G., Helstrom M., Boström H., Li H., Soriano P., Bertholtz C., Heidin C.-H., Alitalo K., Ostman A., Eriksson U.; "PDGF-C is a new protease-activated ligand for the PDGF alpha-receptor.";

RT Nat. Cell Biol. 2:302-309(2000).

RL CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

CC EMBL; AF244813; AAF80597.1; -.

DR Genew; HGNC:8801; PDGFC.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008083; F:growth factor activity; IEA.

DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR00072; PD_growth_factor.

DR Pfam; PF00431; CUB; 1.

DR Pfam; PF00341; PDGF; 1.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS50278; PDGF_2; 1.

DR SEQUENCE 345 AA; 39043 MW; 590889CRA5CC5E8A CRC64;

Query Match 100.0%; Score 1858; DB 4; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.1e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLVTSALAGRGTOAESNLSKQFSSNKQGVDPQHERITITVSTNGSIHS 60
DB 1 MSFGLLVTSALAGRGTOAESNLSKQFSSNKQGVDPQHERITITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLDEPDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLDEPDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQOISKQNOIRIRFVSDXYFPSEPGCIHYNIMVMPQTEAVSPVLPSPA 180
DB 121 GRWCGSGTVPKQOISKQNOIRIRFVSDXYFPSEPGCIHYNIMVMPQTEAVSPVLPSPA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLYRPTMQLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLYRPTMQLLGKAFVGRKSRVVDNL 240
QY 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTCKYHEVQLRPTKTVRGHLSLTVDVALEHHEBCDCVCRGSTGG 345
DB 301 VTCKYHEVQLRPTKTVRGHLSLTVDVALEHHEBCDCVCRGSTGG 345

RESULT 2

Q9UL22 PRELIMINARY; PRT; 345 AA.

AC Q9UL22; PRELIMINARY; PRT; 345 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Secretory growth factor-like protein PALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
GN HSCDGF OR PDGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Tsai Y.-J., Lee R.K.-K., Lin S.-P.;
RT "Pallotein, a novel growth factor like gene identified in human uterus." (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; Pubmed=10858496;
RA Hamada T., Ue-Tai K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; Pubmed=11297552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstetrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a Novel Growth Factor That binds to PDGF alpha and beta Receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF091434; AA00049.1; -;
DR EMBL; AB033831; BAB03266.1; -;
DR EMBL; AF260738; AAK51637.1; -;
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.

DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.5e-172;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLVTSALAGRGTOAESNLSKQFSSNKQGVDPQHERITITVSTNGSIHS 60
DB 1 MSFGLLVTSALAGRGTOAESNLSKQFSSNKQGVDPQHERITITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLDEPDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLDEPDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQOISKQNOIRIRFVSDXYFPSEPGCIHYNIMVMPQTEAVSPVLPSPA 180
DB 121 GRWCGSGTVPKQOISKQNOIRIRFVSDXYFPSEPGCIHYNIMVMPQTEAVSPVLPSPA 180
QY 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLYRPTMQLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLYRPTMQLLGKAFVGRKSRVVDNL 240
QY 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTCKYHEVQLRPTKTVRGHLSLTVDVALEHHEBCDCVCRGSTGG 345
DB 301 VTCKYHEVQLRPTKTVRGHLSLTVDVALEHHEBCDCVCRGSTGG 345

RESULT 3

Q9QY71 PRELIMINARY; PRT; 345 AA.

AC Q9QY71; PRELIMINARY; PRT; 345 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pallotein (Platelet-derived growth factor C).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of fallotein from mouse ovary.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=22354683; Pubmed=12466851;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60, 770 full-length cDNAe.";
RL Nature 420:563-573(2002).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF117608; AAF22516.1; -
DR EMBL; AF266467; AAK58566.1; -
DR EMBL; AK033734; BAC28455.1; -
DR EMBL; AK042767; BAC31358.1; -
DR EMBL; AK052947; BAC35216.1; -
DR MGD; MGI:1859631; Pdgc.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38741 MM; 3A58A1F701B84EA2 CRC64;
Query Match 89.6%; Score 1664; DB 11; Length 345;
Best Local Similarity 86.7%; Pred. No. 3e-154;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;
QY 1 MSFLGLLVTSALAGORRGTQAESNLSSKFPSSNKEQNGVQDPQHERITVSTNGSIHS 60
DB 1 MLLGLLLTSALAGORTGRAESNLSSKLTQSSDKQNGVQDPQHERVITISNGSIHS 60
QY PRPHHTYPRNTVLWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGTL 120
DB 61 PKPHTYPRNVLWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGSL 120
QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEBGFCHYNYVMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEBGFCHYNYVMPQTEAVSPVLPPSS 180
QY 181 LPDLNNNAITAFSTLEDLIRLEPERWQDLLELYRPTWQLGKAFVFGKSRVVDNL 240
DB 181 LSLDLNNNAITAFSTLEDLIRLEPERWQDLLELYRPTWQLGKAFVFGKSRVVDNL 240
QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTITFWPGCLLVRCGNCACCLHNCNCCQVPSK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTITFWPGCLLVRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLOLRPKTGVGKLSLTDVLEHHEBCDCVCRGNAGG 345
DB 301 VTKKYHEVLOLRPKTGVGKLSLTDVLEHHEBCDCVCRGNAGG 345
RESULT 4
Q8C119 PRELIMINARY; PRT; 345 AA.
ID Q8C119
AC Q8C119
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Platelet-derived growth factor, C polypeptide.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CZECH II;
RA Strauberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC037696; AAH37696.1; -
DR MGD; MGI:1859631; Pdgc.
GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38741 MM; 9A58A05C6C0B9614 CRC64;
Query Match 89.5%; Score 1662; DB 11; Length 345;
Best Local Similarity 86.4%; Pred. No. 4.8e-154;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;
QY 1 MSFLGLLVTSALAGORRGTQAESNLSSKFPSSNKEQNGVQDPQHERITVSTNGSIHS 60
DB 1 MLLGLLLTSALAGORTGRAESNLSSKLTQSSDKQNGVQDPQHERVITISNGSIHS 60
QY PRPHHTYPRNTVLWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGTL 120
DB 61 PKPHTYPRNVLWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGSL 120
QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEBGFCHYNYVMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEBGFCHYNYVMPQTEAVSPVLPPSS 180
QY 181 LPDLNNNAITAFSTLEDLIRLEPERWQDLLELYRPTWQLGKAFVFGKSRVVDNL 240
DB 181 LSLDLNNNAITAFSTLEDLIRLEPERWQDLLELYRPTWQLGKAFVFGKSRVVDNL 240
QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTITFWPGCLLVRCGNCACCLHNCNCCQVPSK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTITFWPGCLLVRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLOLRPKTGVGKLSLTDVLEHHEBCDCVCRGNAGG 345
DB 301 VTKKYHEVLOLRPKTGVGKLSLTDVLEHHEBCDCVCRGNAGG 345
RESULT 5
Q9EOX6 PRELIMINARY; PRT; 345 AA.
ID Q9EOX6
AC Q9EOX6
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Missar; TISSUE=Kidney;
RC MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ue-Tel K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to SCDF/PDGF-C/falotin.";
RT Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033830; BAB19969.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.


```
Db 61 PKPHTYRNTVTVLWRLVAVDENWVQLTFDERFGLDEPDDICKYDVEVEBPSDGLVL 120
Qy 121 GRMGSGVPGKQISKGNQIRIRVSDYFSPSEPCFCHYNVWQFPAVSPVLPSPA 180
Db 121 GRMGSSSVPSQISKGNQIRIRVSDYFSPSQPCFCHYTVLWPHTEAPSPSLPSPA 180
Qy 181 LPLDLNNAITAFSTLEDLIRYLEPERWQLEDLYRPTWOLGAFVGRKSRVVDNL 240
Db 181 LPLDLNNAVAGFSTVEELIRYLEPDRWQLEDLYRPTWOLGAFVGRKSRVVDNL 240
Qy 241 LTBEEVRLVSCPRNFVSIRELKTDTTFMPGCLVRCGNCACCLHNCGCVPSK 300
Db 241 LKEEVRVLSCTPRNFVSIRELKTDTTFMPGCLVRCGNCACCHQNCQCIPTK 300
Qy 301 VTKKYHEVLRPKTGVGKSLTDVLAHEHBECDVCRCSTGG 345
Db 301 VTKKYHEVLRPKTGVGKSLTDVLAHEHBECDVCRCSTGG 345
VTKKYHEVLRPKTGVGKSLTDVLAHEHBECDVCRCSTGG 345
```

RESULT 8

```
08K429 PRELIMINARY; PRT; 258 AA.
ID 08K429
AC 08K429;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Goberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
Healing."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF508348; AAM47265.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 29255 MM; 88625B989FC3F8B CRC64;
Query Match 67.8%; Score 1260; DB 11; Length 258;
Best Local Similarity 85.6%; Pred. No. 7.3e-115;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
```

```
Qy 282 GNCACCLHNCGCV 298
Db 241 GNCACCLHNCGCV 257
```

RESULT 9

```
09GZP0 PRELIMINARY; PRT; 370 AA.
ID 09GZP0
AC 09GZP0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SPINAL CORD-derived growth factor-B (MSP036) (IRIS-expressed growth
factor long form) (Platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGFD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Yi-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
SCDF/PDGF-C/fallotxin."
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=iris;
RA Wistow G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881;
RA Bergsten E., Uutela M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Alicata K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
receptor."
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882;
RA Larochele W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF-D, A Novel Protease-Activated Growth Factor."
RL Nat. Cell Biol. 3:517-521(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033832; BAB18903.1; -.
DR EMBL; AF113216; AAC39287.1; -.
DR EMBL; AY027517; AAK20081.1; -.
DR EMBL; AF36376; AAK56136.1; -.
DR EMBL; AF35584; AAK38840.1; -.
DR PIR; JC7591; JC7591.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR InterPro; IPR000531; TonB_box.
DR Pfam; PF00431; CUB; 1.
```


RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numata R., Ono M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Saeki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RU Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 [4]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 [5]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Mech. Enzymol. 303:19-44 (1999).
 [6]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630 (2000).
 [7]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitajima T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaibiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771 (2000).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AF335583; AK38839.1; -
 DR EMBL: AK003359; BAB2735.2; -
 DR MGI: 1919035; Pdgf.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0008083; F:growth factor activity; IEA.
 DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000721; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM0042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SO SEQUENCE 370 AA; 42809 MW; 9580B4CF6813BFBE CRC64;

Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;
 QY 16 QKRTQAESLSKFFQSSKKEQNVOD-PQHERITVSTNGSIHSRFRPTPTVTV 74
 Db 26 QKASIKLARVANR-----RDESNHLDLYQREBNQVTSNGHVQSPFPNSPRNLLT 80
 QY 75 WRLVAEENWVQLTPDERGLDEPDDICKYQFVEVEESDGT--ILGRMGSGTVPGK 132
 Db 81 WMLRS-DEKTRIQSLSPDHQGLBEADICRDPFVEVEESESSTVYRGKMGKHEIPR 139
 QY 133 QISKNQIRIRFVSDVEPSPGFCINYNIMQFTAV-----SPS 174
 Db 140 ITSKTNQIKITFSDVDFVAKPGKITYSFEVDQPEAASETWVESITSSFGVSYHSPS 199
 QY 175 VLPPSALPDLNNAITAEFTEDLIRYLEPERKQDLEDLXPPTWLLGKAPVFGKSR 234
 Db 200 ITDPT-LTPAALPKTVAEPFTVEDLGNFVPMODLENYLDTPHYRSY-HDKSK 257
 QY 235 VVDNLNLTREVRLYSCPTPRNFVSIRELKRTPITFMPGCLVYRCGACACCLHNCNC 294
 Db 258 -VDLDRNDVAKYSCPTPRNHSVNLRELLLTNAVFPFRCILVQRCGACGCGTVMKSC 316
 QY 295 QCVPSKVTXKXHEVLTQLP--KTGVRLKHSJTDVALHEHEBCVCV 339
 Db 317 TCSSGKTVKXKXHEVLTKEPGRKRGKAKMVALVDIDHHEBCDCIC 364
 RESULT 12
 Q9E0T1 PRELIMINARY; PRT; 370 AA.
 ID Q9E0T1
 AC Q9E0T1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Spinal-cord derived growth factor-B.
 GN RSCDGF-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21092670; PubMed=11162582;
 RA Hamada T., Ue-Tai K., Imaki J., Miyata Y.;
 RT "Molecular cloning of SCDF-B, a Novel Growth Factor Homologous to
 RT SCDF/PDEF/C-fallotin";
 RL Biochem. Biophys. Res. Commun. 280:733-737 (2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AB052170; BAB18920.1; -
 DR PIR: JCT592; JCT592.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0008083; F:growth factor activity; IEA.
 DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000721; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM0042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SO SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;
 Query Match 39.7%; Score 736; DB 11; Length 370;
 Best Local Similarity 45.6%; Pred. No. 2,4e-63;
 Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;
 QY 37 EQNGVOD-PQHERITVSTNGSIHSRFRPTPTVTVWRLVAEENWVQLTPDERFG 95
 Db 42 ESNHLDLYRDRNIRRTGTGHVQSPFPNSPRNLLTWRHS-DEKTRIQSLFPHQFG 100
 QY 96 LEDPEDDICKYQFVEVEESDGT--ILGRMGSGTVPGKQISKNQIRIRFVSDVEPSE 153
 Db 101 LBEANDICRYDVEVEEDVSESSTVYRGKMGKHEIPRTSKTNQIKITFQSDDYVAK 160

```

QY 154 PGFCIHNYIV---MPOFTEAV-----SPSVLPSPSALPLDLNNATAFST 195
DB 161 PGFKIYVSFVEDPOPEAASEINWESVTSFSGVSYHSPSW-DSTLADALDAIAAEFD 219
QY 196 LEPLIKLPEERQOLDEDLYRPTWOLGKAFVFGKRSRVVDNLTEERLYSCPTPRNF 255
DB 220 VEDLLKTFNPASQODDLEMLYMDTPRXYGRSY-HERKSK-VLDLRLNDVYKRYSCPTPRNF 277
QY 256 SVSIREELKRTDITFMFGCLLVKRCGNCACCLHNCGCCVPSKVTXKYHEVLOLRP-- 313
DB 278 SVULREELKLTNAVFFRCCLLVORCGNCCGCTLNMKSCCTSSGKTYKATHEVLPFGH 337
QY 314 -KTGVAGLKSITDVALLEHNECDVC 339
DB 338 FKRGRKAKNMALVDIQLDHERCDIC 364

RESULT 13
Q8K2L3 PRELIMINARY; PRT; 261 AA.
AC 08K2L3;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to platelet-derived growth factor, D polypeptide.
GN PDGFD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; BC030896; AA030896.1; -.
DR MGD; MGI:1919035; Pdgfd.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;

Query Match 23.4%; Score 435.5; DB 11; Length 261;
Best Local Similarity 39.8%; Pred. No. 3.9e-34;
Matches 97; Conservative 45; Mismatches 73; Indels 29; Gaps 7;
QY 16 QRRGTQAESNLSSKQFSSNKEQNGVOD-PQHERITVSTNGSIHSPRPPTYPRNTVLY 74
DB 26 QRRSIALRNVANLR-----RDESNHLTDLYOREENIQVTSNGHVQSPRPFNSTPRNLLLT 80
QY 75 MRLVAEENVMYIOLTFDERFGLEDPEDDICKYDFVEEPESDGT--ILGRWGSGGVPPCK 132
DB 81 WMLRS-QEKTRIDLSHDQGLGEAENDICRYDFVEEVESESSIVYVGRMGCHKEIPR 139
QY 133 QISKGNQIRIRFVSDEYFSPSEPGFCIHNYIWPQFTEAV-----SPS 174
DB 140 ITRTQIKITFKSDDYFVAKPGFKLYSFVEDSOPEAASETWSVTSFSGVSYHSPS 199
QY 175 VLPSPALPLDLNNATAFSTLEDLIRYLEPERQOLDEDLYRPTWOLGKAFVFGKRSR 234
DB 200 ITDPT-LTADALDKTVAEPDVEDLKHFNPSWQDLEMLYLDTPHYGRGRSY-HDRKSK 257
QY 235 VVDL 238
DB 258 GIEV 261

RESULT 14
Q8QFX6 PRELIMINARY; PRT; 923 AA.
AC 08QFX6;

```

```

DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Neutrophilin-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RA SEQUENCE FROM N.A.
RA Lee P., Goshl K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
RT "Neutrophilin-1 is required for normal vascular development and is a
RT mediator of VEGF-dependent angiogenesis in zebrafish."
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NEUTROFILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AY064213; AAL40862.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0044872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR008979; Gal Bind like.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_Type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C_2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00022; FA58C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00600; MAM_2; 1.
DR GlycoProtein; Receptor; Transmembrane.
SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA32B2D CRC64;

Query Match 10.3%; Score 190.5; DB 13; Length 923;
Best Local Similarity 27.6%; Pred. No. 2.1e-09;
Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;
QY 5 GLLVTSALAGRRGTQAESNLSSKQFSSNKEQNGVODPQHERITVSTNGSIHSPRP 64
DB 12 GFLVYSALKNDKRCGN-----IRTSANYLTSPGYP 43
QY 65 HTYPRNTVLMRLVAEENVMYIOLTFDERFGLEDPEDDICKYDFVEEPESD--GTLGR 122
DB 44 VVYYSQKCIWITAPGNQRLINPNPHFLEDR--CKDYVEVRDGVDENGQLVCK 100
QY 123 WCGSGTVPKQISKGNQIRIRFVSDEYFSPSEPGFCIHNYIWP-----QFTEAVSPSVL 176
DB 101 YCGK-IAPSPVVSQGNQLIKFVSD-YETHAGGFSIRYEIPFTGPGCSNFTS--SSGV 156
QY 177 PPSALPLDLNNATAFSTLEDLIRYLEPERQOLDEDLYRPTWOLGKAFVFGKRSR 235
DB 157 KSPGPEPKYPNMLDCTFMIFAPKMSIYLFESFELPDTQP-----PAGVCRYDRL 209

RESULT 15
Q8AXP1 PRELIMINARY; PRT; 923 AA.
AC 08AXP1;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Neutrophilin-1.
GN NP-1.

```

OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Shoji W., Tawarayama H.;
RT "The cloning and expression of neuropilin-1";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB088776; BAC53657.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR008979; Gal_Bind_like.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
SQ SEQUENCE 923 AA; 102541 MW; 0E6CE33ED28A21F7 CRC64;

Query March 10.3%; Score 190.5; DB 13; Length 923;
Best Local Similarity 27.6%; Pred. No. 2.1e-09;
Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;

QY 5 GLLIVTSALAGRRGTQAESNLSSKQFSSNKEQNGVDPQHERITVTSTNGSIHSRPF 64
DB 12 GIFLIYVSAALNDKXGDN-----IRITSANYLTSRCYF 43
QY 65 HTVPRNTVLVRLVAVENWITQLTFDERFGLDEPEDDICKYDFVEVEEPPSD--GTLIGR 122
DB 44 VSYTPSOKCIWVITAPGNQRIILINFNPFDLEDRE--CKDYVEVAVDGVENGQLVGK 100
QY 123 WCGSGTVPKQOISKGNQIRIRFVSDEYFPSEPGFCIHNYIMF-----QTEAVSPSVL 176
DB 101 YCGK-IAPSPVSSGNQLFIFVSD-YETHGAGFSIRYEIFKTGPECSRNFPS--SSGVI 156
QY 177 PPSALPIPLDINNATTAFTLEDLIRYLEPERWQLDLEDLYRPTWQLGKAFVGRKSRV 235
DB 157 KSPGPFPEKVRNLDCTFMIFAPKSEIVLEPSEFLEBDTP-----PAGVFCRYDRL 209

Search completed: May 27, 2004, 15:46:42
Job time : 38.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:42:51 ; Search time 16.5 Seconds
(without alignments)
1079.452 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848
Sequence: 1 MLLGLLLLSALAGQRTG.....DVALEHHECDVCVCGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTCUS COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilee1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	4 US-09-457-066-43	Sequence 43, Appl
2	1848	100.0	345	4 US-09-564-595D-35	Sequence 35, Appl
3	1848	100.0	345	4 US-09-706-968-43	Sequence 43, Appl
4	1848	100.0	345	4 US-09-823-033-4	Sequence 4, Appl
5	1667	90.2	345	4 US-09-040-220D-2	Sequence 2, Appl
6	1667	90.2	345	4 US-09-457-066-2	Sequence 2, Appl
7	1667	90.2	345	4 US-09-265-686-2	Sequence 2, Appl
8	1667	90.2	345	4 US-09-540-224-5	Sequence 5, Appl
9	1667	90.2	345	4 US-09-564-595D-33	Sequence 33, Appl
10	1667	90.2	345	4 US-09-706-968-2	Sequence 2, Appl
11	1667	90.2	345	4 US-09-723-749-2	Sequence 2, Appl
12	1667	90.2	345	4 US-09-823-033-2	Sequence 2, Appl
13	1204.5	65.2	303	4 US-09-564-595D-57	Sequence 57, Appl
14	1200	64.9	302	4 US-09-564-595D-54	Sequence 54, Appl
15	1035.5	56.0	317	4 US-09-564-595D-56	Sequence 56, Appl
16	1019	55.1	316	4 US-09-564-595D-55	Sequence 55, Appl
17	752	40.7	370	4 US-09-457-066-37	Sequence 37, Appl
18	752	40.7	370	4 US-09-540-224-2	Sequence 2, Appl
19	752	40.7	370	4 US-09-564-595D-2	Sequence 2, Appl
20	752	40.7	370	4 US-09-706-968-37	Sequence 37, Appl
21	752	40.7	370	4 US-09-808-972-2	Sequence 2, Appl
22	752	40.7	370	4 US-09-823-033-5	Sequence 5, Appl
23	746.5	40.4	370	4 US-09-540-224-4	Sequence 4, Appl
24	746.5	40.4	370	4 US-09-564-595D-53	Sequence 53, Appl
25	746.5	40.4	370	4 US-09-808-972-4	Sequence 4, Appl
26	185	10.0	1015	4 US-09-285-385C-2	Sequence 2, Appl
27	183	9.9	1012	4 US-09-285-385C-4	Sequence 4, Appl

28	181	9.8	788	1 US-08-572-225-1	Sequence 1, Appl
29	181	9.8	986	4 US-09-285-385C-19	Sequence 19, Appl
30	177.5	9.6	730	3 US-08-872-757-2	Sequence 2, Appl
31	177.5	9.6	730	4 US-09-850-048A-2	Sequence 2, Appl
32	176	9.5	923	4 US-09-439-711C-2	Sequence 2, Appl
33	176	9.5	923	4 US-09-583-638-2	Sequence 2, Appl
34	175	9.5	101	3 US-09-374-135-6	Sequence 6, Appl
35	172	9.3	922	4 US-09-116-473-4	Sequence 4, Appl
36	169	9.1	923	3 US-08-936-135-6	Sequence 6, Appl
37	169	9.1	923	4 US-09-439-711C-6	Sequence 6, Appl
38	168	9.1	921	4 US-09-439-711C-4	Sequence 4, Appl
39	168	9.1	986	3 US-08-872-757-4	Sequence 4, Appl
40	168	9.1	986	4 US-09-850-048A-4	Sequence 4, Appl
41	165	8.9	1013	2 US-08-866-650-3	Sequence 3, Appl
42	165	8.9	1013	2 US-09-021-287-3	Sequence 3, Appl
43	165	8.9	1013	3 US-09-240-473-3	Sequence 3, Appl
44	162	8.8	591	3 US-08-991-408-4	Sequence 4, Appl
45	162	8.8	591	4 US-09-432-473-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-09-457-066-43
Sequence 43, Application US/09457066
Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZYGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 43
LENGTH: 345
TYPE: PRT
ORGANISM: Mus musculus
US-09-457-066-43

Query Match      100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.1e-195;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
   1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
DQ 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
   1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
QY 61 PKRPHYPRAMVYVWRIVANDENVRIQLTDERFGLEDPDDIDCKDFVVEEESDGSVL 120
   61 PKRPHYPRAMVYVWRIVANDENVRIQLTDERFGLEDPDDIDCKDFVVEEESDGSVL 120
DQ 61 PKRPHYPRAMVYVWRIVANDENVRIQLTDERFGLEDPDDIDCKDFVVEEESDGSVL 120
   61 PKRPHYPRAMVYVWRIVANDENVRIQLTDERFGLEDPDDIDCKDFVVEEESDGSVL 120
QY 121 GRMGSGTVGKQTSKGNHRIKRFVSDEYPSRPGFCIHYSIMPQVTEETSPSPVLPSS 180
   121 GRMGSGTVGKQTSKGNHRIKRFVSDEYPSRPGFCIHYSIMPQVTEETSPSPVLPSS 180
DQ 121 GRMGSGTVGKQTSKGNHRIKRFVSDEYPSRPGFCIHYSIMPQVTEETSPSPVLPSS 180
   121 GRMGSGTVGKQTSKGNHRIKRFVSDEYPSRPGFCIHYSIMPQVTEETSPSPVLPSS 180
QY 181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSLYPTWQLLGAFLYKSKSRVNLNT 240
   181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSLYPTWQLLGAFLYKSKSRVNLNT 240
DQ 181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSLYPTWQLLGAFLYKSKSRVNLNT 240
   181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSLYPTWQLLGAFLYKSKSRVNLNT 240
QY 241 LKEEVLYSCTPKNFSVSTSEELIKRTDTTWPCGLVKRGGNACACCHNCCQCVPRK 300
   241 LKEEVLYSCTPKNFSVSTSEELIKRTDTTWPCGLVKRGGNACACCHNCCQCVPRK 300
DQ 241 LKEEVLYSCTPKNFSVSTSEELIKRTDTTWPCGLVKRGGNACACCHNCCQCVPRK 300
   241 LKEEVLYSCTPKNFSVSTSEELIKRTDTTWPCGLVKRGGNACACCHNCCQCVPRK 300
QY 301 VTKKYHEVLTLPRTGVKGLHKLTDVALEHHECDVCVCGNAGG 345
   301 VTKKYHEVLTLPRTGVKGLHKLTDVALEHHECDVCVCGNAGG 345
```

Db 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345

RESULT 2

Sequence 35, Application US/09564595D

Patent No. 6495668

GENERAL INFORMATION:

APPLICANT: Gilbert, Teresa

APPLICANT: Hart, Charles E.

APPLICANT: Shepherd, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REFERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

PRIOR FILING DATE: 2000-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 60/164,463

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FaastSeq for Windows Version 4.0

SEQ ID NO 35

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-564-595D-35

Query Match

Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 Db 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 QY 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 Db 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 QY 181 LSLDLNNNAVTAFTSTEEILRIYLEPPRMQVDDLSLYKPTWOLLGKAFVIGKSKVNNLNL 240
 181 LSLDLNNNAVTAFTSTEEILRIYLEPPRMQVDDLSLYKPTWOLLGKAFVIGKSKVNNLNL 240
 Db 181 LSLDLNNNAVTAFTSTEEILRIYLEPPRMQVDDLSLYKPTWOLLGKAFVIGKSKVNNLNL 240
 QY 241 LKEEVVLYSCTPRNFVSIRBELKRTDTTFMPCGLLVKRCGNCACCLHNCNECQCVPK 300
 241 LKEEVVLYSCTPRNFVSIRBELKRTDTTFMPCGLLVKRCGNCACCLHNCNECQCVPK 300
 Db 241 LKEEVVLYSCTPRNFVSIRBELKRTDTTFMPCGLLVKRCGNCACCLHNCNECQCVPK 300
 QY 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345
 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345
 Db 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345

RESULT 3

US-09-706-968-43

Sequence 45, Application US/09706968

Patent No. 6528050

GENERAL INFORMATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Piddington, Christopher S.

APPLICANT: Shepherd, Paul O.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

FILE REFERENCE: 98-60C1

CURRENT APPLICATION NUMBER: US/09/706, 968

CURRENT FILING DATE: 2000-11-06

PRIOR APPLICATION NUMBER: US/09/541, 752

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 43

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-706-968-43

Query Match

Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 Db 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 QY 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 Db 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 QY 181 LSLDLNNNAVTAFTSTEEILRIYLEPPRMQVDDLSLYKPTWOLLGKAFVIGKSKVNNLNL 240
 181 LSLDLNNNAVTAFTSTEEILRIYLEPPRMQVDDLSLYKPTWOLLGKAFVIGKSKVNNLNL 240
 Db 181 LSLDLNNNAVTAFTSTEEILRIYLEPPRMQVDDLSLYKPTWOLLGKAFVIGKSKVNNLNL 240
 QY 241 LKEEVVLYSCTPRNFVSIRBELKRTDTTFMPCGLLVKRCGNCACCLHNCNECQCVPK 300
 241 LKEEVVLYSCTPRNFVSIRBELKRTDTTFMPCGLLVKRCGNCACCLHNCNECQCVPK 300
 Db 241 LKEEVVLYSCTPRNFVSIRBELKRTDTTFMPCGLLVKRCGNCACCLHNCNECQCVPK 300
 QY 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345
 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345
 Db 301 VTKKHEVLQLRPKTVGKGLHKSLLTDVALEHHBECDCVCRGNAGG 345

RESULT 4

US-09-823-033-4

Sequence 4, Application US/09823033

Patent No. 6663870

GENERAL INFORMATION:

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

FILE REFERENCE: 00-12

CURRENT APPLICATION NUMBER: US/09/823, 033

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-823-033-4

Query Match

Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 Db 1 MLILGLLLTSLAAGRTGTRAESNLSSKQLQSSDKEQGVDPHRRVVTISGNGSIHS 60
 QY 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 Db 61 PKPHTYPRNMVLWRLVAVDENVRQLTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPPSPGFCIHSIIMPQVETTSPPSVLPSS 180

```

Db      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345

```

RESULT 5
US-09-040-220D-2
Sequence 2, Application US/09040220D
Patent No. 6393311

```

GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
FILE REFERENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040.220D
CURRENT FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-040-220D-2

```

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 5.5e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

```

      1 MLLGLLLITSLAAGRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
      1 MSLEGLLLITSLAAGRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
      61 PKPHTYPRMVLVWRLVAVDENVRIQLTDERFGLEDPEDDICKYDFVEVEEPPSDGVL 120
      61 PRFHTYPRMVLVWRLVAVDENVRIQLTDERFGLEDPEDDICKYDFVEVEEPPSDGVL 120
      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345

```

RESULT 6
US-09-457-066-2
Sequence 2, Application US/09457066
Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Geo. Zeren
APPLICANT: Hart, Charles E.

```

APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457.066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-066-2

```

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 5.5e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

```

      1 MLLGLLLITSLAAGRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
      1 MSLEGLLLITSLAAGRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60
      61 PKPHTYPRMVLVWRLVAVDENVRIQLTDERFGLEDPEDDICKYDFVEVEEPPSDGVL 120
      61 PRFHTYPRMVLVWRLVAVDENVRIQLTDERFGLEDPEDDICKYDFVEVEEPPSDGVL 120
      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRMGSGTVPGKQSKGNHRIKRVSDPEYFSEPGFCHHSIIMPQVETTSPEVLPPSS 180
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAAVTAFTSEELIRYLEPDRWQVLDLSLYPTWQLGKAPLYGKSKRYVNL 240
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTITFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345
      301 VTKKYHEVLQLRPTGVGKGLHKSITDVALHHEBECDCVCAGNAG 345

```

RESULT 7
US-09-265-686-2
Sequence 2, Application US/09265686
Patent No. 6455283
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGY TO VEGF AND BMP1
FILE REFERENCE: P1122P2
CURRENT APPLICATION NUMBER: US/09/265.686
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040.220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184.216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-265-686-2

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 5.5e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

```

      1 MLLGLLLITSLAAGRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60

```


PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-706-968-2

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 5.5e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLAGORTGRTAENSLSKQLSDKXNGVODPRHREVTITSGNGSHS 60
DB 1 MSLFGLLLTSLAGORGTQAESNLSSKQFSSNKENGVDQDQHERIITVSTNGSHS 60
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGSVL 120
DB 61 PRPHITPRNTVLVWRLVAVBENWIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEBGFCHYSIIMPQVETTSPPSVLPSS 180
DB 121 GRWCGSGTVPKGQTSKGNQIRIRFVSDEYFPSEBGFCHYNIIMPQTEAVSPSVLPSSA 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVODLSLYKPTWQLGKAFYGGKSKVYNLNTL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPDRQVODLSLYKPTWQLGKAFVFGKSKRVVDLNTL 240
QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIMPGLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTBVRILYSCTPRNFVSIRBELKRTDTIIMPGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLHKSITDVALBHEBECDCVCRGNAG 345
DB 301 VTKKYHEVLQLRPKTVGVLHKSITDVALBHEBECDCVCRGSTG 345

RESULT 11
US-09-723-749-2
Sequence 2, Application US/09723749
Patent No. 6620784
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
FILE REFERENCE: P1122P2D1
CURRENT APPLICATION NUMBER: US/09/723,749
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-723-749-2

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 5.5e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLAGORTGRTAENSLSKQLSDKXNGVODPRHREVTITSGNGSHS 60
DB 1 MSLFGLLLTSLAGORGTQAESNLSSKQFSSNKENGVDQDQHERIITVSTNGSHS 60
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGSVL 120
DB 61 PRPHITPRNTVLVWRLVAVBENWIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120

DB 61 PRPHITPRNTVLVWRLVAVBENWIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEBGFCHYSIIMPQVETTSPPSVLPSS 180
DB 121 GRWCGSGTVPKGQTSKGNQIRIRFVSDEYFPSEBGFCHYNIIMPQTEAVSPSVLPSSA 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVODLSLYKPTWQLGKAFYGGKSKVYNLNTL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPDRQVODLSLYKPTWQLGKAFVFGKSKRVVDLNTL 240
QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIMPGLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTBVRILYSCTPRNFVSIRBELKRTDTIIMPGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLHKSITDVALBHEBECDCVCRGNAG 345
DB 301 VTKKYHEVLQLRPKTVGVLHKSITDVALBHEBECDCVCRGSTG 345

RESULT 12
US-09-823-033-2
Sequence 2, Application US/09823033
Patent No. 6663870
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-033-2

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 5.5e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLAGORTGRTAENSLSKQLSDKXNGVODPRHREVTITSGNGSHS 60
DB 1 MSLFGLLLTSLAGORGTQAESNLSSKQFSSNKENGVDQDQHERIITVSTNGSHS 60
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGSVL 120
DB 61 PRPHITPRNTVLVWRLVAVBENWIOITPDERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEBGFCHYSIIMPQVETTSPPSVLPSS 180
DB 121 GRWCGSGTVPKGQTSKGNQIRIRFVSDEYFPSEBGFCHYNIIMPQTEAVSPSVLPSSA 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVODLSLYKPTWQLGKAFYGGKSKVYNLNTL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPDRQVODLSLYKPTWQLGKAFVFGKSKRVVDLNTL 240
QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIMPGLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTBVRILYSCTPRNFVSIRBELKRTDTIIMPGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLHKSITDVALBHEBECDCVCRGNAG 345
DB 301 VTKKYHEVLQLRPKTVGVLHKSITDVALBHEBECDCVCRGSTG 345

RESULT 13
US-09-564-595D-57
Sequence 57, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:

```

APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZW6GF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 303
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

```

Query Match	65.2%	Score 1204.5	DB 4	Length 303
Best Local Similarity	71.3%	Pred. 120.43e-124		
Matches 216	Conservative 42	Mismatches 40	Indels 5	Gaps 3
Qy	47	ERVVITSGNGSIHSPKPHPTYPNMYLVWRLVAVDENVRIQLTFDERPGLDEPDDICTKY	106	
Db	2	DEITQYKGVNGYVQSPFPFNSYPRNLLTWRLHS-QENTRIQLVFQNGGLEAENDICTY	60	
Qy	107	DPFVEVEPBDGVL--GRWCSSGYTPGKOTSXGNHIRIRFVSDEYFSPSPFCIHSIT-	163	
Db	61	DPEVEEDISSTIIIRGWCGRKEVEPRKSTNQDIKTFKSDSYFAKPKPFKIYSLLE	120	
Qy	164	-MEQVETTESPSVLPSSSLDLDLNNAAVAFSTLEELIRYIEPPRMQVLDLSYKPPMOL	222	
Db	121	DFPPAAASVSPSVLPSPALPDLNNALTAFTSTLEDLIRIIEPPEMQDLEDLYPTMOL	180	
Qy	223	LGRAPLYGKKSQVNLNLKEBEVKYSTCPNFSVSIREELKRTDTITFWPQCILVYKCG	282	
Db	181	LGRAPVFGKRSRVNDNLITTEVRLYSCTPNFSVSIREELKRTDTITFWPQCILVYKCG	240	
Qy	283	NCACCLIANNECCQVPRKVTYKTYHEVLTQRPYTGXGLHSLTDVALBHHEECDQVCRN	342	
Db	241	NCACCLIANNECCQVPSKYTKKYHEVLTQRPYTGXGLHSLTDVALBHHEECDQVCRGS	300	
Qy	343	AGG	345	
Db	301	TGG	303	

```

RESULT 14
US-09-564-595D-54
; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZWGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54

```

```

; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

```

Query Match	64.9%	Score 1200	DB 4	Length 302
Best Local Similarity	72.4%	Pred. No. 1.3e-123		
Matches 215, Conservative	35	Mismatches 43	Indels 4	Gaps 2

Qy	46	HEWVIVISGNQSIHSHKPFHTYPRMVLVWMLVADEVNRQLTFDRFRGLDEBDDIC	105
Db	1	HEHIIIVSNGSIHSHRPFHTYPRVTVLWMLVAEEVWVQLTFDRFRGLDEBDDIC	60
Qy	106	YDFVEVEEPEDSVLGRWGSGTVDPKOTSGKNHRIREFVDEYFPESEPGFCHYSTIMP	165
Db	61	YDFVEVEEESDGTIIIGRWGSGGTVGAKOISKNOAIRFVDEYFPESEPGFCHYNIWMP	120
Qy	166	QVETTESPVLPSPSSLDLNNATARSTLEILRYLPEPRKQVDDLSLYKPMWLLGK	225
Db	121	QFHEAVSPVLPSPSALPFDLLNNATATASSTIEDLRYLPEPRKQVDDLEDLRYPMWLLGK	180
Qy	226	APLYGKKSRYVNLNLKEEVLKYSTPRNFVSIRBELKRTDITFWEGCLLYKRCGNCA	285
Db	181	APFVFGKSR-VDLDRINDAKRYSCTPRNYSVNIREEKLNVFPPRCCLLYGCGNCG	239
Qy	286	CCILHNEGQCPRKYTKKYEHEVQLAR--KTVGKGLKSLTGVALLDHHHEECQVC	339
Db	240	CGTVNRRSCTCNSGKTVKKEHEVQLFEGHIIKRRKQATKMLVDIQLDHNERCCQIC	296

```

; RESULT 15
; US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6493668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZWCSF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ. ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
; US-09-564-595D-56

```

[illegible]

Db 121 DFQPAASETWESVTSISGVSYNPSVTD P-TLIADALDKIAEFDTVEDLKYFNP 179
QY 207 RMQVLDLSLYKPTWQLGKAFLYGKSKVYNLNLKEEVLKYSCTPRNFSYSIRBELKRT 266
Db 180 SMOEDLENMYLDTPRYGRSY-HDRKSKVVDLNLTEEVLKYSCTPRNFSYSIRBELKRT 238
QY 267 DTIFWPGCLVYKRCGNCACCLHNCNECQCVPRKYTKKYHEVLQLRPKTGVLHKS LTD 326
Db 239 DTIFWPGCLVYKRCGNCACCLHNCNECQCVPSKYTKKYHEVLQLRPKTGVLHKS LTD 298
QY 327 VALEHHEBCDCVCRGNAGG 345
Db 299 VALEHHEBCDCVCRGSTGG 317

Search completed: May 27, 2004, 15:48:09
Job time : 17.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:46:47 ; Search time 39 Seconds

(without alignments)
2470.284 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848
Sequence: 1 MLLLGILLTSALAGRTGT.....DVLEHHECDVCGRNAGG 345

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep:*

5: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/2/pubppaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*

8: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*

10: /cgn2_6/prodata/2/pubppaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/prodata/2/pubppaa/US09C_NEW_PUB.pep:*

13: /cgn2_6/prodata/2/pubppaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/prodata/2/pubppaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep:*

17: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

18: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	9	US-09-823-033-4
2	1848	100.0	345	9	US-09-818-943-2
3	1848	100.0	345	9	US-09-852-209A-7
4	1848	100.0	345	11	US-09-876-813-35
5	1848	100.0	345	12	US-10-664-432-4
6	1848	100.0	345	12	US-10-439-337A-7
7	1848	100.0	345	12	US-10-303-997B-7
8	1848	100.0	345	13	US-10-139-583-43
9	1848	100.0	345	14	US-10-131-600-7
10	1848	100.0	345	14	US-10-264-361-4
11	1667	90.2	345	9	US-09-823-033-2
12	1667	90.2	345	9	US-09-923-995-4
13	1667	90.2	345	9	US-09-795-006A-149
14	1667	90.2	345	9	US-09-978-295A-488
15	1667	90.2	345	9	US-09-978-697-488

16	1667	90.2	345	9	US-09-978-192A-488	Sequence 488, App
17	1667	90.2	345	9	US-09-999-832A-488	Sequence 488, App
18	1667	90.2	345	10	US-09-978-189-488	Sequence 488, App
19	1667	90.2	345	10	US-09-796-753-6	Sequence 6, Appl1
20	1667	90.2	345	10	US-09-978-608A-488	Sequence 488, App
21	1667	90.2	345	10	US-09-978-585A-488	Sequence 488, App
22	1667	90.2	345	10	US-09-978-191A-488	Sequence 488, App
23	1667	90.2	345	10	US-09-978-403A-488	Sequence 488, App
24	1667	90.2	345	10	US-09-978-564A-488	Sequence 488, App
25	1667	90.2	345	10	US-09-999-833A-488	Sequence 488, App
26	1667	90.2	345	10	US-09-981-915A-488	Sequence 488, App
27	1667	90.2	345	10	US-09-978-824A-488	Sequence 488, App
28	1667	90.2	345	10	US-09-918-585A-488	Sequence 488, App
29	1667	90.2	345	10	US-09-978-423A-488	Sequence 488, App
30	1667	90.2	345	10	US-09-978-193A-488	Sequence 488, App
31	1667	90.2	345	10	US-09-999-830A-488	Sequence 488, App
32	1667	90.2	345	10	US-09-978-757A-488	Sequence 488, App
33	1667	90.2	345	10	US-09-978-187A-488	Sequence 488, App
34	1667	90.2	345	10	US-09-978-643A-488	Sequence 488, App
35	1667	90.2	345	10	US-09-978-375A-488	Sequence 488, App
36	1667	90.2	345	10	US-09-978-298A-488	Sequence 488, App
37	1667	90.2	345	10	US-09-978-188A-488	Sequence 488, App
38	1667	90.2	345	10	US-09-978-681A-488	Sequence 488, App
39	1667	90.2	345	10	US-09-978-194A-488	Sequence 488, App
40	1667	90.2	345	10	US-09-999-829A-488	Sequence 488, App
41	1667	90.2	345	10	US-09-978-299A-488	Sequence 488, App
42	1667	90.2	345	10	US-09-978-544A-488	Sequence 488, App
43	1667	90.2	345	10	US-09-978-665A-488	Sequence 488, App
44	1667	90.2	345	10	US-09-978-802A-488	Sequence 488, App
45	1667	90.2	345	11	US-09-876-813-33	Sequence 33, Appl1

ALIGNMENTS

RESULT 1

US-09-823-033-4

Sequence 4, Application US/09823033

Patent No. US2002004225A1

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

FILE REFERENCE: 00-12

CURRENT FILING DATE: 2001-03-03

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-823-033-4

Query Match 100.0%; Score 1848; DB 9; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.3e-173;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLLGILLTSALAGRTGTGRTASNNLSKQLQSSDKQNGVOPRHRVVTISNGSIHS 60

DB 1 MLLLGILLTSALAGRTGTGRTASNNLSKQLQSSDKQNGVOPRHRVVTISNGSIHS 60

QY 61 PKPHTYPRNMVWLVAVDENVRIQLTDERFGLEDPPDDICKYDFVEBPSDSVL 120

DB 61 PKPHTYPRNMVWLVAVDENVRIQLTDERFGLEDPPDDICKYDFVEBPSDSVL 120

QY 121 GRNGSGTVGKQTSKKNHRIKRVSDYRPPSPGCFIHSIIMPOTETTSRSLPPSS 180

DB 121 GRNGSGTVGKQTSKKNHRIKRVSDYRPPSPGCFIHSIIMPOTETTSRSLPPSS 180

QY 181 LSLDLNNAVTAASSTLEELTRYLLEPPDMQVLDLSLYPTQGLGKAFLYKKSKSVVNLN 240

Db 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLKYPTWOLLGKAFLYGKSKVNNL 240
 QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRCGACCLHNCNCCQCVPRK 300
 Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRCGACCLHNCNCCQCVPRK 300
 QY 301 VTKKYEVLQLRPKTGKGLHKSLLTDVLEHHEBCDCCVCRGNAGG 345
 Db 301 VTKKYEVLQLRPKTGKGLHKSLLTDVLEHHEBCDCCVCRGNAGG 345

RESULT 2

US-09-818-943-2
 ; Sequence 2, Application US/09818943
 ; Patent No. US20020043987A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ERIKSSON, Ulf
 ; APPLICANT: LI, Xuri
 ; APPLICANT: PONTEN, Annica
 ; APPLICANT: AASE, Karin
 ; APPLICANT: LI, Hong
 ; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
 ; TITLE OF INVENTION: (PFC-C) AND USES THEREOF
 ; FILE REFERENCE: 1064/48487
 ; CURRENT APPLICATION NUMBER: US/09/818,943
 ; CURRENT FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: US 60/192,507
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 345
 ; TYPE: PRF
 ; ORGANISM: Murinae gen. sp.
 US-09-818-943-2

Query Match 100.0%; Score 1848; DB 9; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.3e-173;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGTRASNLSKQLQSSDKXQGVDPHRRVVTTSNGSHS 60
 Db 1 MLILGLLLTSLAAGRTGTRASNLSKQLQSSDKXQGVDPHRRVVTTSNGSHS 60
 QY 61 PKFPHTPRNMYLVRLVAVDENVRQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
 Db 61 PKFPHTPRNMYLVRLVAVDENVRQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
 Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
 QY 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLKYPTWOLLGKAFLYGKSKVNNL 240
 Db 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLKYPTWOLLGKAFLYGKSKVNNL 240
 QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRCGACCLHNCNCCQCVPRK 300
 Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRCGACCLHNCNCCQCVPRK 300
 QY 301 VTKKYEVLQLRPKTGKGLHKSLLTDVLEHHEBCDCCVCRGNAGG 345
 Db 301 VTKKYEVLQLRPKTGKGLHKSLLTDVLEHHEBCDCCVCRGNAGG 345

RESULT 3

US-09-852-209A-7
 ; Sequence 7, Application US/09852209A
 ; Patent No. US20020164687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ERIKSSON, Ulf
 ; APPLICANT: AASE, Karin
 ; APPLICANT: LEE, Xuri

APPLICANT: PONTEN, Annica
 APPLICANT: TUTTELA, Marko
 APPLICANT: ALITALO, Kari
 APPLICANT: OESTMAN, Arne
 APPLICANT: HELDIN, Carl-Henrik
 APPLICANT: BETHSHOLTZ, Christer
 TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
 TITLE OF INVENTION: THEREFOR, AND USES THEREOF
 FILE REFERENCE: 09-410349-eriksson et al-1064-44740
 CURRENT APPLICATION NUMBER: US/09/852,209A
 CURRENT FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: 09/410,349
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: 60/110,749
 PRIOR FILING DATE: 1998-12-03
 PRIOR APPLICATION NUMBER: 60/113,002
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 60/135,426
 PRIOR FILING DATE: 1999-05-21
 PRIOR APPLICATION NUMBER: 60/144,022
 PRIOR FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 7
 LENGTH: 345
 TYPE: PRF
 ORGANISM: Murinae gen. sp.
 US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 9; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.3e-173;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGTRASNLSKQLQSSDKXQGVDPHRRVVTTSNGSHS 60
 Db 1 MLILGLLLTSLAAGRTGTRASNLSKQLQSSDKXQGVDPHRRVVTTSNGSHS 60
 QY 61 PKFPHTPRNMYLVRLVAVDENVRQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
 Db 61 PKFPHTPRNMYLVRLVAVDENVRQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
 Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
 QY 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLKYPTWOLLGKAFLYGKSKVNNL 240
 Db 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLKYPTWOLLGKAFLYGKSKVNNL 240
 QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRCGACCLHNCNCCQCVPRK 300
 Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRCGACCLHNCNCCQCVPRK 300
 QY 301 VTKKYEVLQLRPKTGKGLHKSLLTDVLEHHEBCDCCVCRGNAGG 345
 Db 301 VTKKYEVLQLRPKTGKGLHKSLLTDVLEHHEBCDCCVCRGNAGG 345

RESULT 4

US-09-876-813-35
 ; Sequence 35, Application US/09876813
 ; Publication No. US20040002140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilbert, Teresa
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPA
 ; FILE REFERENCE: 99-19
 ; CURRENT APPLICATION NUMBER: US/09/876,813
 ; PRIOR APPLICATION NUMBER: US/09/564,595
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/304,216

PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 345
TYPE: PRT
ORGANISM: Mus musculus
US-09-876-813-35

Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSAAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60
DB 1 MLLIGLLLTSAAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
DB 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBPGFCIHYSIIMPQVETETSPSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBPGFCIHYSIIMPQVETETSPSVLPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAPLYGKSKSVNLT 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAPLYGKSKSVNLT 240
QY 241 LKEEVKLYSCTPRNFSVSIREFLKRDTTIFFPGCLLYKRCGNCACCLHNCQCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREFLKRDTTIFFPGCLLYKRCGNCACCLHNCQCVPRK 300
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345

RESULT 5
US-10-664-432-4
Sequence 4, Application US/10664432
Publication No. US20040043031A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/10/664,432
CURRENT FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 345
TYPE: PRT
ORGANISM: Mus musculus
US-10-664-432-4

Query Match 100.0%; Score 1848; DB 12; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLIGLLLTSAAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60
DB 1 MLLIGLLLTSAAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
DB 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBPGFCIHYSIIMPQVETETSPSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBPGFCIHYSIIMPQVETETSPSVLPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAPLYGKSKSVNLT 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAPLYGKSKSVNLT 240
QY 241 LKEEVKLYSCTPRNFSVSIREFLKRDTTIFFPGCLLYKRCGNCACCLHNCQCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREFLKRDTTIFFPGCLLYKRCGNCACCLHNCQCVPRK 300
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345

RESULT 6
US-10-439-337A-7
Sequence 7, Application US/10439337A
Publication No. US20040053837A1
GENERAL INFORMATION:
APPLICANT: LI, Xuri
APPLICANT: ERIKSSON, Ulf
APPLICANT: CARMELET, Peter
TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND
FILE REFERENCE: 029065,44740C4
CURRENT APPLICATION NUMBER: US/10/439,337A
CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 10/303,997
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 60/102,461
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: US 60/108,109
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: US 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: US 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 345
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-439-337A-7

Query Match 100.0%; Score 1848; DB 12; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLIGLLLTSAAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60
DB 1 MLLIGLLLTSAAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
DB 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBPGFCIHYSIIMPQVETETSPSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBPGFCIHYSIIMPQVETETSPSVLPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAPLYGKSKSVNLT 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAPLYGKSKSVNLT 240

```

Db      181  LSLIDLNNAVTAFTSTBELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLNL 240
Qy      241  LKEEVKLVSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300
Db      241  LKEEVKLVSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300
Qy      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345
Db      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 7
US-10-303-997B-7
; Sequence 7, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303, 997B
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRK
; ORGANISM: Murinae gen. sp.
US-10-303-997B-7

Query Match      100.0%; Score 1848; DB 12; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLLGLLLTSLAAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60
Db      1  MLLGLLLTSLAAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60
Qy      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Db      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Qy      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Db      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Qy      121  GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180
Db      121  GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180
Qy      181  LSLIDLNNAVTAFTSTBELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLNL 240
Db      181  LSLIDLNNAVTAFTSTBELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLNL 240
Qy      241  LKEEVKLVSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300
Db      241  LKEEVKLVSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300
Qy      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345
Db      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345

```

```

Db      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 8
US-10-139-583-43
; Sequence 43, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRK
; ORGANISM: Mus musculus
US-10-139-583-43

Query Match      100.0%; Score 1848; DB 13; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLLGLLLTSLAAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60
Db      1  MLLGLLLTSLAAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60
Qy      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Db      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Qy      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Db      61  PKPHTYPRNMVLYWMLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGSYL 120
Qy      121  GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180
Db      121  GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180
Qy      181  LSLIDLNNAVTAFTSTBELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLNL 240
Db      181  LSLIDLNNAVTAFTSTBELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLNL 240
Qy      241  LKEEVKLVSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300
Db      241  LKEEVKLVSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300
Qy      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345
Db      301  VTKKHEVLOLRPKTGKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 9
US-10-131-600-7
; Sequence 7, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christler
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

```


TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/10/131,600
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/108,109
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 345
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-131-600-7

Query Match 100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 1,3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGRTAESNLSSKQLSDKEONGVODPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLITLSALAGORTGRTAESNLSSKQLSDKEONGVODPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRMGSGTVPGKOTSKGNHIRIRFVSDYFPSEBPGFCHYSIIMPQVETTSPTVLPSS 180
DB 121 GRMGSGTVPGKOTSKGNHIRIRFVSDYFPSEBPGFCHYSIIMPQVETTSPTVLPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLT 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLT 240
QY 241 LKEEVKLYSCTPRNFSVSIREBLKRTDTTFWPGCLVYRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREBLKRTDTTFWPGCLVYRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCVCRGNAGG 345
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCVCRGNAGG 345

RESULT 10
US-10-264-361-4
Sequence 4, Application US/10264361
Publication No. US20030087870a1
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
FILE REFERENCE: 00-53
CURRENT APPLICATION NUMBER: US/10/264,361
PRIOR FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: US/09/695,121
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 345
TYPE: PRT
ORGANISM: Mus musculus
US-10-264-361-4

Query Match 100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 1,3e-173;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGRTAESNLSSKQLSDKEONGVODPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLITLSALAGORTGRTAESNLSSKQLSDKEONGVODPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRMGSGTVPGKOTSKGNHIRIRFVSDYFPSEBPGFCHYSIIMPQVETTSPTVLPSS 180
DB 121 GRMGSGTVPGKOTSKGNHIRIRFVSDYFPSEBPGFCHYSIIMPQVETTSPTVLPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLT 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLT 240
QY 241 LKEEVKLYSCTPRNFSVSIREBLKRTDTTFWPGCLVYRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREBLKRTDTTFWPGCLVYRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCVCRGNAGG 345
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCVCRGNAGG 345

RESULT 11
US-09-823-033-2
Sequence 2, Application US/09823033
Patent No. US2002004225A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-033-2

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 9.9e-156;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGRTAESNLSSKQLSDKEONGVODPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLITLSALAGORTGRTAESNLSSKQLSDKEONGVODPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRMGSGTVPGKOTSKGNHIRIRFVSDYFPSEBPGFCHYSIIMPQVETTSPTVLPSS 180
DB 121 GRMGSGTVPGKOTSKGNHIRIRFVSDYFPSEBPGFCHYSIIMPQVETTSPTVLPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLT 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLT 240
QY 241 LKEEVKLYSCTPRNFSVSIREBLKRTDTTFWPGCLVYRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREBLKRTDTTFWPGCLVYRCGNCACCLHNCNECCVPRK 300

QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEBCDVCVRGNAG 345
 Db 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEBCDVCVRGNAG 345

RESULT 12
 US-09-923-995-4
 ; Sequence 4, Application US/09923995
 ; Patent No. US20020081700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shepard, Paul O
 ; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNKL
 ; FILE REFERENCE: 00-47
 ; CURRENT APPLICATION NUMBER: US/09/923,995
 ; CURRENT FILING DATE: 2001-08-07
 ; PRIOR APPLICATION NUMBER: US 60/223,164
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-923-995-4

Query Match 90.2%; Score 1667; DB 9; Length 345;
 Best Local Similarity 87.0%; Pred. No. 9,9e-156;
 Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGRTGTRAESNLSSKLTQSSDKQNGVDPRIHRRVVTISGNSIHS 60
 Db 1 MSIFGLLLTSALAGRGQTQAESNLSSKFPSSNKEQNGVDPQHERITTVSTNGSIHS 60
 QY 61 PKPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGYL 120
 Db 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDEDDICXDFVEVEEPPSDGYL 120
 QY 121 GRWCGSTVPKQTSKGNHRIKRVSDPEPSEPGFCIHYSIMPQVETTSFVLPSS 180
 Db 121 GRWCGSTVPKQTSKGNQIRIFVSDPEPSEPGFCIHYNIMPQTEAVSPVLPSS 180
 QY 181 LSLDLNNAVTAFTSEELIRYLEPDRWQVDLSLYKPTMOLIGKAFYGGKSRVVDNL 240
 Db 181 LPDDLNNAITAFSTEDLIRYLEPDRWQVDLSLYKPTMOLIGKAFVFGKSRVVDNL 240
 QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLVYKRCGNACCLHNCNECCVPRK 300
 Db 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLVYKRCGNACCLHNCNECCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEBCDVCVRGNAG 345
 Db 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEBCDVCVRGNAG 345

RESULT 13
 US-09-795-006A-149
 ; Sequence 149, Application US/09795006A
 ; Patent No. US20020151680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altaleo et al
 ; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
 ; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
 ; FILE REFERENCE: 28967/35977B
 ; CURRENT APPLICATION NUMBER: US/09/795,006A
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: US 60/205,331
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 60/185,205
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 149
 ; LENGTH: 345

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-795-006A-149

Query Match 90.2%; Score 1667; DB 9; Length 345;
 Best Local Similarity 87.0%; Pred. No. 9,9e-156;
 Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGRTGTRAESNLSSKLTQSSDKQNGVDPRIHRRVVTISGNSIHS 60
 Db 1 MSIFGLLLTSALAGRGQTQAESNLSSKFPSSNKEQNGVDPQHERITTVSTNGSIHS 60
 QY 61 PKPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLEDEDDICXDFVEVEEPPSDGYL 120
 Db 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDEDDICXDFVEVEEPPSDGYL 120
 QY 121 GRWCGSTVPKQTSKGNHRIKRVSDPEPSEPGFCIHYSIMPQVETTSFVLPSS 180
 Db 121 GRWCGSTVPKQTSKGNQIRIFVSDPEPSEPGFCIHYNIMPQTEAVSPVLPSS 180
 QY 181 LSLDLNNAVTAFTSEELIRYLEPDRWQVDLSLYKPTMOLIGKAFYGGKSRVVDNL 240
 Db 181 LPDDLNNAITAFSTEDLIRYLEPDRWQVDLSLYKPTMOLIGKAFVFGKSRVVDNL 240
 QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLVYKRCGNACCLHNCNECCVPRK 300
 Db 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLVYKRCGNACCLHNCNECCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEBCDVCVRGNAG 345
 Db 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEBCDVCVRGNAG 345

RESULT 14
 US-09-978-295A-488
 ; Sequence 488, Application US/09978295A
 ; Patent No. US2002015606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aeshkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250

[illegible]

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 9,9e-156;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLGLGLTSLAGORTGRASNSLSKQLSDKQNGVDPBRRVVTISGNSIHS 60
DB 1 MSFGLLLTSLAGOGQAGQASNSLSKQFSSNKEQNGVDPBRRITVTSNGSIHS 60
QY 61 PKRPHTYPRNMVLMWRLVAVDENVRQLTFDERFGLDEPDIDCKYDFVEEPPSDGSYL 120
DB 61 PRPHYPRNTVLMWRLVAVDENVRQLTFDERFGLDEPDIDCKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRIPVSDYPPSPGFCIHSIMPOVETTSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHIRIPVSDYPPSPGFCIHSIMPOVETTSVLPSS 180
QY 181 LSLDLNNATVASTBELRYLEPDRQVLDLSIKPMTQLGKAFLYGKSKVYNTL 240
DB 181 LSLDLNNATVASTBELRYLEPDRQVLDLSIKPMTQLGKAFLYGKSKVYNTL 240
QY 241 LKEEVLYSCPTPNFSVIREELKRTDTTFWPGCLVYKCGNACCLHNHCNCCQCVPRK 300
DB 241 LKEEVLYSCPTPNFSVIREELKRTDTTFWPGCLVYKCGNACCLHNHCNCCQCVPRK 300
QY 301 VTKKYEHLQLRPKTVGKGLHKSLLTVALEHHECCVCCGNAGG 345
DB 301 VTKKYEHLQLRPKTVGKGLHKSLLTVALEHHECCVCCGNAGG 345

RESULT 15
US-09-978-697-488
Sequence 488, Application US/09978697
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334

; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081071
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081819
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081952
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082700
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-23
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083495
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083496
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083499
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083554
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083558
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083559
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083500
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083742
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084598
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.28; Score 1667; DB 9; Length 345;

Best Local Similarity 87.06; Pred. No. 9.9e-156; Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLILTLTALAGRTGRASNLSSKQLSDSKQNGVODPRHRVVTISGNGSIHS 60
 Db 1 MSLLGLILTLTALAGRTGRASNLSSKQLSDSKQNGVODPRHRVVTISGNGSIHS 60
 Qy 61 PKPHTYPRNVTVMRLVAVDENVRITLTDERFGLEDPEDDICTKPFVEEESDGSVL 120
 Db 61 PRPHTYPRNVTVMRLVAVDENVRITLTDERFGLEDPEDDICTKPFVEEESDGSVL 120
 Qy 121 GRWGSSTVPKQSKQNRIRIPVSDYFPPSEBFCIHYSIIMPOVTEITSPVLPPSS 180
 Db 121 GRWGSSTVPKQSKQNRIRIPVSDYFPPSEBFCIHYSIIMPOVTEITSPVLPPSS 180
 Qy 181 LSLDLNNAVTAESTLEELIRYLEPDRQVLDLSYKPTQLGKAFLYGKSKRYVNLNL 240
 Db 181 LPLDLNNAVTAESTLEELIRYLEPDRQVLDLSYKPTQLGKAFVPRKSKRYVNLNL 240
 Qy 241 LKEEVKLYSCTPRNFSVISIEELKRTDTITWPGCLVRCGAGCACCLANCNCCQVPRK 300
 Db 241 LKEEVKLYSCTPRNFSVISIEELKRTDTITWPGCLVRCGAGCACCLANCNCCQVPSK 300
 Qy 301 VTKKXHEVLDLRPTGVGLHKSITDVALHHEBCDVCVCGNNG 345
 Db 301 VTKKXHEVLDLRPTGVGLHKSITDVALHHEBCDVCVCGSTG 345

Search completed: May 27, 2004, 15:56:27
Job time : 40 secs

This Page Blank (uspto)

ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor. PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C. PDGF-C can also be used to regulate the receptor-binding specificity of PDGF-C. PDGF-C can also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, mesarkyblastic leukaemia, lung carcinoma and erythroleukemia, can be identified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions, especially found in the lung, kidney or liver

Query Match	Similarity	100.0%	Score 1848	DB 3	Length 345
Best Local	Similarity	100.0%	Pred. No. 1.8e-181		
Matches 345	Conservative	0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MLLLGLLLTSLALGORTGTTRAESNLSSKLTQLSDKENGQVODPRIHERVVTISGNCSIHS	60		
Db	1	MLLLGLLLTSLALGORTGTTRAESNLSSKLTQLSDKENGQVODPRIHERVVTISGNCSIHS	60		
Qy	61	PKPFTTYPRNNVLVRLVAVDENNRIQLTFDERFGLDEPDDICKYDFVEVEBSPDSGYL	120		
Db	61	PKPFTTYPRNNVLVRLVAVDENNRIQLTFDERFGLDEPDDICKYDFVEVEBSPDSGYL	120		
Qy	121	GRMGSGVPGQKQTSKGNHRIIRFVSDEFPSBPBGCHYSIIMPOVETTSBSYLPPSS	180		
Db	121	GRMGSGVPGQKQTSKGNHRIIRFVSDEFPSBPBGCHYSIIMPOVETTSBSYLPPSS	180		
Qy	181	LSLDLNNAAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTMOLLGKAFLYGKSKSVNNLN	240		
Db	181	LSLDLNNAAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTMOLLGKAFLYGKSKSVNNLN	240		
Qy	241	LKEEYKLYSCTPRNFSVSIRBELKRTDTIIFWPGCLIVKCGGACACCLHNCEQCVPKR	300		
Db	241	LKEEYKLYSCTPRNFSVSIRBELKRTDTIIFWPGCLIVKCGGACACCLHNCEQCVPKR	300		
Qy	301	VTKKKHEVLTQLRPKTGVKGLHSLTDVALAHHHEECQVCVRGNAG	345		
Db	301	VTKKKHEVLTQLRPKTGVKGLHSLTDVALAHHHEECQVCVRGNAG	345		

	AA96861	AA96861 standard; protein; 345 AA.
RESULT 2		
ID	AA96861	
XX	AA96861	
AC		
XX		
DT	26-SEP-2000 (first entry)	
XX		
DE	Murine vascular endothelial growth factor homologue, ZVEGF3.	
XX		
XX	Vascular endothelial growth factor; homologue; zvegf3; CUB domain.	
KW	Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;	
KW	chromosome 4q28.3; cytosolic; anti-psoriatic; anti-inflammatory;	
KW	anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;	
KW	vulnerary.	
XX		
XX		
OS	Mus musculus.	
XX		
PN	WO200034474-A2.	
XX		
PD	15-JUN-2000.	
XX		
PF	07-DEC-1999; 99WO-US028968.	

XX 07-DEC-1998; 98US-00207120.
PR 06-JUL-1989; 99US-0142576P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
XX
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
XX
PI Gao Z, Hart CB, Piddington CS, Shepard PO, Shoemaker KB;
PI Gilbertson DG, West JW;
XX
XX WPI; 2000-423420/36.
DR N-PSDB; AAA51527.
XX
XX Novel zvegf3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence.
XX
PS Claim 1; Page 169-170; 173pp; English.

CC This shows a murine ZVEGF3, a novel vascular endothelial growth factor
CC homologue. Polypeptides comprising an epitope-bearing portion human or
CC murine ZVEGF3 are claimed. The growth factors comprise a growth factor
CC domain and a CUB domain (genetic sequence motifs are shown in AAY96839
CC and AAY96860). The growth factor domain is characterized by an
CC arrangement of cysteine residues and beta-strands that is characteristic
CC of the "cysteine knot" structure of the platelet-derived growth factor
CC (PDGF) family. The CUB domain shows homology to CUB domains in
CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
CC protein, bovine acidic seminal fluid protein and Xenopus laevis collid-
CC like protein. Structural analysis and homology predict that ZVEGF3
CC polypeptides complex with a second polypeptide to form multimeric
CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.
CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
CC muscle cells, for activating cell surface PDGF-alpha receptor and for
CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
CC useful for regulating (post-development) organ growth, regeneration and
CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
CC antagonists are useful for treating cancer, rheumatoid arthritis,
CC diabetic retinopathy, ischemic limb disease, peripheral vascular disease,
CC myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound
CC healing, chronic liver disease and haemangioma formation. ZVEGF3 can also
CC be used to modulate neurite growth and development of the nervous system,
CC and for treating neurodegenerative diseases

Query Match	100.0%	Score 1848	DB 3	Length 345
Best Local Similarity	100.0%	Pred. No. 1.8e-181		
Matches 345	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MLLGLLLTTSALAGORTGRTAESNLSSKQLQSSDPKEQNGVDPREHREVITISGNGSIHS	60	
Db	1	MLLGLLLTTSALAGORTGRTAESNLSSKQLQSSDPKEQNGVDPREHREVITISGNGSIHS	60	
QY	61	PKPHTTYRNNVLYWRLVAVDENVRILTPEBRRLPEBDDICRYDVEVEBESDGSYL	120	
Db	61	PKPHTTYRNNVLYWRLVAVDENVRILTPEBRRLPEBDDICRYDVEVEBESDGSYL	120	
QY	121	GRMGCSGVPGKQTSKGNHIRIRFVSDSEFPSEPGFCIHYSIIMPQVETTSPSVLPPSS	180	
Db	121	GRMGCSGVPGKQTSKGNHIRIRFVSDSEFPSEPGFCIHYSIIMPQVETTSPSVLPPSS	180	
QY	181	LSLDLNNNAVTAFSTLEEILRYLEBDRQVQVLDLSLYKFTWQLGKALFYGKSKRVNVLNL	240	
Db	181	LSLDLNNNAVTAFSTLEEILRYLEBDRQVQVLDLSLYKFTWQLGKALFYGKSKRVNVLNL	240	
QY	241	LKEEVKLYSCSPRRPVSIVIRELKRDTDTIPMPGCLVVRGGNACCLHNCGECQVPRK	300	
Db	241	LKEEVKLYSCSPRRPVSIVIRELKRDTDTIPMPGCLVVRGGNACCLHNCGECQVPRK	300	
QY	301	VTKKYHEVTLQLRPTYGVKGLHKSLTDVALHEHHEEDCVCRGNAGG	345	

Db 301 VTKKYHEVLQLRPKTVGKGLHKSLTDVALBHHBECDCVCRGNAG 345

RESULT 3
AAB48658
ID AAB48658 standard; protein; 345 AA.
XX
AC AAB48658;
XX
DT 09-MAR-2001 (first entry)
XX
DE Mouse zvegf3, SEQ ID NO:35.
XX
KM Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;
KM murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;
KM neovascularization; tissue repair; proliferation; differentiation;
KM liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KM periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KM immunomodulation; hepatic.
XX
OS Mus musculus.
XX
PN WO20006736-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US040047.
XX
PR 03-MAY-1999; 99US-00304216.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
DR WPI: 2000-687541/67.
DR N-PSDB: AAC81583.
XX
PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease.
XX
PS Disclosure: Page 130-131; 143pp; English.
XX
CC The invention relates to the human growth factor homologue zvegf4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
CC fusions; expression constructs and host cells comprising human zvegf4
CC nucleic acids; the recombinant expression of human zvegf4; an antibody
CC which binds to human zvegf4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method
CC of modulating the proliferation, differentiation, migration or metabolism
CC of bone cells, comprising exposing bone cells to zvegf4-derived
CC polypeptides; and a method of detecting a genetic abnormality in the
CC zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be
CC used to stimulate tissue development or repair, or cellular
CC differentiation or proliferation. They are particularly used for the
CC treatment or repair of liver damage, and may also be used to modulate
CC neurite growth (e.g., in the treatment of Alzheimer's disease or multiple
CC sclerosis). Due to their osteogenic activity, they may be used in the
CC treatment of periodontal disease and fractures. They may also be used to
CC enhance expansion and mobilisation of haematopoietic stem cells and
CC endothelial precursor stem cells, which may be useful in the treatment of
CC ischaemia, in wound healing, and in the modulation of the immune system.
CC The present sequence represents mouse zvegf3

XX
SQ Sequence 345 AA;
Query Match 100.0%; Score 1848; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 1,8e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLILTSALAGRTGRABSNLSKQLQSDSKQNGVQDRHRVVTISNGSIS 60
DB 1 MLILGLILTSALAGRTGRABSNLSKQLQSDSKQNGVQDRHRVVTISNGSIS 60
QY 61 PKPHTYPRNMVAVRVAADENVRQLTFDERGLEDPEDDICKYDFVEVEBPSDSYL 120
DB 61 PKPHTYPRNMVAVRVAADENVRQLTFDERGLEDPEDDICKYDFVEVEBPSDSYL 120
QY 121 GRWCGSGTVPQKQTSKNNHRIREFSDEYRPPSEPGFCIHYSIIMPQVETTSPEVLPPSS 180
DB 121 GRWCGSGTVPQKQTSKNNHRIREFSDEYRPPSEPGFCIHYSIIMPQVETTSPEVLPPSS 180
QY 181 LSLDLNNAVTAPESTLELRYLEPDRNOVDLSLYPTWQLGKAFLYGKKSRYVNLNL 240
DB 181 LSLDLNNAVTAPESTLELRYLEPDRNOVDLSLYPTWQLGKAFLYGKKSRYVNLNL 240
QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIPGCLIVKRCGNCACCLHNCNQCVPYRK 300
DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIIPGCLIVKRCGNCACCLHNCNQCVPYRK 300
QY 301 VTKKYHEVLQLRPKTVGKGLHKSLTDVALBHHBECDCVCRGNAG 345
DB 301 VTKKYHEVLQLRPKTVGKGLHKSLTDVALBHHBECDCVCRGNAG 345

RESULT 4
AAE00998
ID AAE00998 standard; protein; 345 AA.
XX
AC AAE00998;
XX
DT 04-JUL-2001 (first entry)
XX
DE Mouse zvegf3 protein.
XX
KM Mouse; zvegf3 antagonist; cell proliferation; stellate cell activation;
KM extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
KM platelet-derived growth factor; PDGF; vascular endothelial growth factor;
KM VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
KM chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
KM diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
KM asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
KM diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
KM pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
KM bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
KM fibroproliferative disorder.
XX
OS Mus musculus.
XX
PN WO200128586-A1.
XX
DR 26-APR-2001.
XX
PF 23-OCT-2000; 2000WO-US029270.
XX
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
PR 01-AUG-2000; 2000US-0222233P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbertson DG;
XX
DR WPI: 2001-300278/31.
DR N-PSDB: AAD04650.
XX

PT Use of zvegf3 antagonist for reducing fibroproliferative disorder of
PT kidney, liver and bone, reducing extracellular matrix production,
PT creating fibrosis or reducing stellate cell activation in mammal.
XX
XX Example 2; Fig 2; 70pp; English.
XX
CC The patent discloses materials and methods for reducing cell
CC proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a Zvegf3 antagonist in combination
CC with a delivery vehicle. The Zvegf3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The Zvegf3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the
CC mitogenic effects of Zvegf3 and thereby to inhibit or prevent and treat
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
CC antitrypsin deficiency, fibrotic disorders of the kidney such as
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancreas, fibroproliferative disorders of the
CC vasculature such as transplant vasculopathy and fibroproliferative
CC disorders of the bone such as osteopetrosis and hyperostosis. The present
CC sequence is mouse Zvegf3 protein
XX
XX
SQ Sequence 345 AA;
Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.8e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLTLTALAGORTGRASNLSSKQLSSDKONQVOPRHRVVTIGNSIHS 60
DB 1 MLLGLLTLTALAGORTGRASNLSSKQLSSDKONQVOPRHRVVTIGNSIHS 60
QY 61 PKRPHYPRNMVLMRLVAVDENVRQLTDFERFGLDEPDDICXKDFVEEPPSDGSYL 120
DB 61 PKRPHYPRNMVLMRLVAVDENVRQLTDFERFGLDEPDDICXKDFVEEPPSDGSYL 120
QY 121 GRMGSGCTVPKQKTSKGNHRIKRVSDYRPPSEPGCIHYSITMPQVETTSFVLPSS 180
DB 121 GRMGSGCTVPKQKTSKGNHRIKRVSDYRPPSEPGCIHYSITMPQVETTSFVLPSS 180
QY 181 LSLDLNNATATSTLEIRLEPRWQVLDLSYKPTQLGKAFVYKSKRVNVLN 240
DB 181 LSLDLNNATATSTLEIRLEPRWQVLDLSYKPTQLGKAFVYKSKRVNVLN 240
QY 241 LKEEVLKYSCTPRNFVSIREELKRTDTIFWPGCLAVKRCGNCACCLHNKNCQCVPK 300
DB 241 LKEEVLKYSCTPRNFVSIREELKRTDTIFWPGCLAVKRCGNCACCLHNKNCQCVPK 300
QY 301 VTKKYEHLVQLRPTGVKGLHKSITDVALHHEBCDVCNGNAG 345
DB 301 VTKKYEHLVQLRPTGVKGLHKSITDVALHHEBCDVCNGNAG 345
RESULT 5
ABG92894 standard; protein; 345 AA.
XX
AC ABG92894;
XX
DT 19-NOV-2002 (first entry)
XX
DE Mouse VEGF-like protein zvegf 3.
XX
KM VEGF; vascular endothelial growth factor; zvegf 3; mouse; chromosome 3;
KM cell proliferation; differentiation; metabolism; migration;
KM revascularization; solid tumour; diabetic retinopathy; psoriasis;
KM rheumatoid arthritis; cancer; autoimmune disease; inflammation;
KM myocardial ischaemia; scleroderma; fibrosis; glomerulosclerosis;

KW atherosclerosis; skin wound; ulcer; burn; skin grafting;
KW female reproductive tract disorder; chronic liver disease;
KW circulatory disorder; heart failure; neurodegenerative disease;
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
KW neurite outgrowth.
XX
XX Mus musculus.
XX
XX US6432673-B1.
XX
XX 13-ANG-2002.
XX
XX 07-DEC-1999; 99US-00457066.
XX
XX 07-DEC-1998; 98US-0111173P.
XX
XX 06-JUL-1999; 99US-0142576P.
XX
XX 21-OCT-1999; 99US-0161653P.
XX
XX 12-NOV-1999; 99US-0165255P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
XX Gilbertson DG, West JW;
XX
XX WPI; 2002-689759/74.
XX
XX N-PSDB; ABS68648.
XX
XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,
XX ulcers, burns, skin grafting, female reproductive tract disorders,
XX Parkinson's disease, and Alzheimer's disease.
XX
XX Example 4; Fig 2; 68pp; English.
XX
XX The invention relates to an isolated polypeptide, designated zvegf3 (a
XX vascular endothelial growth factor-like protein) of 11-136 amino acid
XX residues in length and comprises the sequence appearing as ABG9289 from
XX amino acid residues 235-345. Also included are an isolated protein
XX comprising a first polypeptide disulphide bonded to a second polypeptide,
XX where each of the first and second polypeptides is from zvegf 3, and
XX where the protein modulates cell proliferation, differentiation,
XX metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3
XX expression vectors and host cells. Zvegf 3 is useful as additives in
XX tissue adhesives for promoting revascularisation of the healing tissue,
XX for designing molecules that antagonise semaphorin-stimulated activities,
XX including neurite growth, cardiovascular development, cartilage and limb
XX development, and T and B-cell function, and for imaging tumours or other
XX sites of abnormal cell proliferation and in gene therapy applications.
XX The proteins are useful therapeutically to stimulate tissue development
XX or repair, or cellular differentiation or proliferation, for stimulating
XX the growth of fibroblast or smooth muscle cells, as molecular weight
XX standards, as reagents in assays for determining circulatory level of the
XX protein or as standards in the analysis of cell phenotype, for
XX identifying inhibitors of their activity which are useful for reducing
XX the growth of solid tumours, for treating diabetic retinopathy,
XX psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune
XX disease, inflammation, myocardial ischaemia, scleroderma, and reducing
XX fibrosis, including scar formation, keloids, liver fibrosis, lung
XX fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including
XX diabetic nephropathy), glomerulosclerosis, atherosclerosis, skin wounds,
XX ulcers, burns, skin grafting, and female reproductive tract disorders,
XX chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's
XX disease, circulatory disorders e.g. heart failure, hepatic or portal vein
XX thrombosis, cardiac sclerosis, neurodegenerative diseases such as
XX multiple sclerosis, Parkinson's disease, Alzheimer's disease, and for
XX regenerating neurite outgrowth following strokes. The gene for mouse
XX zvegf3 is located on chromosome 3. The present sequence represents zvegf
XX 3
XX
SQ Sequence 345 AA;
Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.8e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLLIGLLILTSALAGORTGTGRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60
 1 MLLIGLLILTSALAGORTGTGRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60
 Db 1 MLLIGLLILTSALAGORTGTGRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60
 Qy 61 PKPHTYPRMVLVWRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEEBSDSVL 120
 61 PKPHTYPRMVLVWRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEEBSDSVL 120
 Db 61 PKPHTYPRMVLVWRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEEBSDSVL 120
 Qy 121 GRMGSGTVGKQTSKGNHRIKRVSDPEYPSRPGCFIHYSIIMPQVETSTSPVLPPSS 180
 121 GRMGSGTVGKQTSKGNHRIKRVSDPEYPSRPGCFIHYSIIMPQVETSTSPVLPPSS 180
 Db 121 GRMGSGTVGKQTSKGNHRIKRVSDPEYPSRPGCFIHYSIIMPQVETSTSPVLPPSS 180
 Qy 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240
 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240
 Db 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240
 Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFMPGCLVYKRCGNCACCLHNCNCCQVPRK 300
 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFMPGCLVYKRCGNCACCLHNCNCCQVPRK 300
 Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFMPGCLVYKRCGNCACCLHNCNCCQVPRK 300
 Qy 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345
 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345

RESULT 6
 AAB47890
 ID AAB47890 standard; protein; 345 AA.
 AC AAB47890;
 XX 12-FEB-2002 (first entry)
 DT Mouse platelet-derived growth factor (PDGF-C) protein.
 DE Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;
 KM cardiac hypertrophy; fibrosis.
 XX Mus sp.
 OS WO200172132-A1.
 PN 04-OCT-2001.
 PD 28-MAR-2001; 2001WO-US009855.
 PE 28-MAR-2000; 2000US-0192507P.
 PR (LUDW-) LUDWIG INST CANCER RES.
 PA Eriksson U, Li X, Ponten A, Aase K, Li H;
 PI WPI; 2002-010700/01.
 DR A transgenic animal over-expressing platelet derived growth factor C is
 PT useful to study and find therapy for disease associated with PDGF-C over-
 PT expression, including cardiac hypertrophy and fibrosis.
 PT Example 4; Page 42-43; 48pp; English.
 PS The patent discloses a method for producing a transgenic, non-human
 XX animal over-expressing a platelet derived growth factor C (PDGF-C), or
 CC its functional fragment or analogue. The method involves introducing a
 CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the
 CC cell into a non-human animal and allowing the cell to develop into a
 CC transgenic, non-human animal. The transgenic animal is useful as a model
 CC to study disease states characterised by over-expression of PDGF-C and to
 CC find therapy for those diseases, particularly hypertrophy and fibrosis in
 CC various organs including the heart. The present sequence is PDGF-C
 CC protein from mouse
 XX Sequence 345 AA;
 SQ

Query Match 100.0%; Score 1848; DB 5; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.8e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLIGLLILTSALAGORTGTGRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60
 1 MLLIGLLILTSALAGORTGTGRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60
 Db 1 MLLIGLLILTSALAGORTGTGRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60
 Qy 61 PKPHTYPRMVLVWRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEEBSDSVL 120
 61 PKPHTYPRMVLVWRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEEBSDSVL 120
 Db 61 PKPHTYPRMVLVWRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEEBSDSVL 120
 Qy 121 GRMGSGTVGKQTSKGNHRIKRVSDPEYPSRPGCFIHYSIIMPQVETSTSPVLPPSS 180
 121 GRMGSGTVGKQTSKGNHRIKRVSDPEYPSRPGCFIHYSIIMPQVETSTSPVLPPSS 180
 Db 121 GRMGSGTVGKQTSKGNHRIKRVSDPEYPSRPGCFIHYSIIMPQVETSTSPVLPPSS 180
 Qy 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240
 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240
 Db 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240
 Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFMPGCLVYKRCGNCACCLHNCNCCQVPRK 300
 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFMPGCLVYKRCGNCACCLHNCNCCQVPRK 300
 Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFMPGCLVYKRCGNCACCLHNCNCCQVPRK 300
 Qy 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345
 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345

RESULT 7
 AAB47890
 ID AAB47890 standard; protein; 345 AA.
 AC AAB47890;
 XX 16-MAY-2002 (first entry)
 DT Mouse zvegf3.
 DE Human; mouse; zvegf3; zvegf4; platelet derived growth factor; PDGF;
 KM homolog; growth; bone; ligament; cartilage; proliferation; osteoblast;
 KM chondrocyte; bony defect; fracture; bone graft; implant;
 KM periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.
 XX Mus musculus.
 OS US200204225-A1.
 PN 10-JAN-2002.
 PD 29-MAR-2001; 2001US-00823033.
 PE 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 PR 31-MAR-2000; 2000US-0193723P.
 PA (HART/) HART C E.
 PI (GILB/) GILBERTSON D G.
 PI Hart CE, Gilbertson DG;
 DR WPI; 2002-171026/22.
 DR N-PSDB; AAI72444.
 XX Promoting growth of bone, ligament or cartilage in a mammal, involves
 XX administering to the mammal a protein which comprises growth factor
 PT domain of zvegf3 protein, a homolog of platelet-derived growth factor.
 XX Claim 1; Page 19-20; 31pp; English.
 PS

XX The sequences given in ABA47889-90 represent human and mouse zvegf3, respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog and it was used in the method of the invention for promoting growth of bone, ligament or cartilage and stimulating proliferation of osteoblasts or chondrocytes in a mammal. The proteins used were preferably a dimeric protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3 protein, with a delivery vehicle. The method of the invention is useful for promoting growth of bone, ligament or cartilage in a mammal, where the composition is administered at a site of a bony defect, preferably a fracture, bone graft site, implant site, or periodontal pocket, and for stimulating proliferation of osteoblasts or chondrocytes in a mammal. It is further useful for promoting proliferation of osteoblasts, osteoclasts, chondrocytes or bone marrow stem cells, where the bone marrow stem cells are harvested from a patient prior to culture. The method is therefore useful for treating osteoporosis

SO Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.8e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVDPHRRVTTISGNGSIHS 60
DB 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVDPHRRVTTISGNGSIHS 60
QY 61 PKPHTYPRNMVLMVRLVAVDENVRIOQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
DB 61 PKPHTYPRNMVLMVRLVAVDENVRIOQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIKRVSDYEPSEPGFCIHYSIIMPOVETTSPSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIKRVSDYEPSEPGFCIHYSIIMPOVETTSPSVLPSS 180
QY 181 LSLDLNNATATSTLEELIRLEPRMVDLSYKPTWQLGKAPLYKKSKVNNL 240
DB 181 LSLDLNNATATSTLEELIRLEPRMVDLSYKPTWQLGKAPLYKKSKVNNL 240
QY 241 LKEEVLVYSGTPRNFSVSIREELEKRTDTTFMPCGLVYKRCGNCACCLHNCNCCQVPRK 300
DB 241 LKEEVLVYSGTPRNFSVSIREELEKRTDTTFMPCGLVYKRCGNCACCLHNCNCCQVPRK 300
QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 8
ABU72435
ID ABU72435 standard; protein; 345 AA.
XX
AC ABU72435;
XX
DT 16-JUN-2003 (first entry)
XX
DE Mouse ZVEGF4-related protein #1.
XX
KW Growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;
KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease.
XX
OS Mus musculus.
XX
PN US6495668-B1.
XX
PD 17-DEC-2002.
XX
PF 03-MAY-2000; 2000US-00564595.

XX 03-MAY-1999; 99US-0132250P.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Gilbert T, Hart CE, Shepard PO, Gilbertson DG;
XX
DR WPI: 2003-352153/33.
DR N-PSDB; ACA64117.
XX
PT Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
PS Disclosure; Col 95-98; 67pp; English.

CC The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homodimers or heterodimers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. A transgene construct was made for producing mice transgenic for
CC human ZVEGF4. The construct contained human growth hormone gene control
CC regions. The present sequence is a ZVEGF4-related protein sequence. Note:
CC The present sequence is included in the sequence listing but is not
CC mention elsewhere in the specification

SO Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.8e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVDPHRRVTTISGNGSIHS 60
DB 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVDPHRRVTTISGNGSIHS 60
QY 61 PKPHTYPRNMVLMVRLVAVDENVRIOQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
DB 61 PKPHTYPRNMVLMVRLVAVDENVRIOQLTFDERFGLEDPEDDICXKDFVEVEPSDGSYL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIKRVSDYEPSEPGFCIHYSIIMPOVETTSPSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIKRVSDYEPSEPGFCIHYSIIMPOVETTSPSVLPSS 180
QY 181 LSLDLNNATATSTLEELIRLEPRMVDLSYKPTWQLGKAPLYKKSKVNNL 240
DB 181 LSLDLNNATATSTLEELIRLEPRMVDLSYKPTWQLGKAPLYKKSKVNNL 240
QY 241 LKEEVLVYSGTPRNFSVSIREELEKRTDTTFMPCGLVYKRCGNCACCLHNCNCCQVPRK 300
DB 241 LKEEVLVYSGTPRNFSVSIREELEKRTDTTFMPCGLVYKRCGNCACCLHNCNCCQVPRK 300
QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 9
 ABG76398
 ID ABG76398 standard; protein, 345 AA.
 XX
 AC ABG76398;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Mouse growth factor homologue, zvegf3.
 XX
 KM Mouse; growth factor homologue; zvegf3; fibroblast; smooth muscle cell;
 KM full-thickness platelet-derived growth factor alpha receptor; PDGF;
 KM prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
 KM revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
 KM chronic active hepatitis; hepatic chronic passive congestion; stroke;
 KM central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;
 KM portal vein thrombosis; cardiac sclerosis; new vessel formation;
 KM endothelial precursor stem cell; neovascularisation; wound healing;
 KM organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
 KM sensory neurite outgrowth; brain damage; head injury; paralysis;
 KM spinal injury; neurodegenerative disease; diabetic retinopathy;
 KM psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
 KM lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
 KM proliferative vascular disorder; ocular neovascularisation;
 KM inflammatory disorder; rheumatoid arthritis; vasculogenesis;
 KM angiogenesis; nervous system disorder; cytostatic; hepatotropic;
 KM vlnetary; tranquilliser; cerebroprotective; neuroprotective; nootropic;
 KM ophthalmological; dermatological; coagulant; cardiant.
 XX
 OS Mus musculus.
 XX
 PN US2002177193-A1.
 PD 28-NOV-2002.
 XX
 PF 02-MAY-2002; 2002US-00139583.
 XX
 PR 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gao Z, Hart CE, Piddington CS, Shepard PO, Shoemaker KB;
 PI Gilbertson DG, West JW;
 XX
 DR WPI, 2003-328485/31.
 DR N-PSDB; ABX93182.
 XX
 PT New isolated zvegf3 polypeptide, useful for treating cancer, Alzheimer's
 PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein
 PT thrombosis, comprises growth factor domain and CUB domain.
 XX
 PS Claim 1; Fig 6; 73pp; English.
 XX
 CC The present invention relates to the isolation of a growth factor
 CC homologue referred to as zvegf3, and the polynucleotide sequence encoding
 CC it. The zvegf3 polypeptide is useful for stimulating the growth of
 CC fibroblasts or smooth muscle cells, or for activating a cell-surface
 CC platelet-derived growth factor (PDGF) alpha receptor. The zvegf3
 CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
 CC for treating full-thickness skin wounds, female reproductive tract and
 CC prolonged bleeding, periodontal disease, damaged liver tissue, and
 CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
 CC adhesives for promoting revascularisation of healing tissue. The zvegf3
 CC polypeptide is also useful for treating liver damage including damage due
 CC to liver disease, chronic active hepatitis, hepatic chronic passive
 CC congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein

thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
 CC cirrhosis. The polypeptide is useful for enhancing expansion and
 CC mobilisation of endothelial precursor stem cells, creating and
 CC stabilising new vessel formation in areas requiring neovascularisation,
 CC including areas of ischaemia, organ transplants, wound healing, and
 CC tissue grafting. It may be used for treating peripheral neuropathies by
 CC increasing spinal cord and sensory neurite outgrowth, and as part of
 CC therapeutic treatment for the regeneration of neurite outgrowths
 CC following strokes, brain damage caused by head injuries, and paralysis
 CC caused by spinal injuries. Application may also be made in treating
 CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
 CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
 CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
 CC zvegf3 is useful for blocking the mitogenic, chemotactic, or angiogenic
 CC effects of zvegf3, and for treating proliferative vascular disorders,
 CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
 CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
 CC and diseases of the nervous system. The present sequence represents mouse
 CC zvegf3
 XX
 SQ Sequence 345 AA;
 XX
 Query Match 100.0%; Score 1848; DB 6; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1,8e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLILGILLITSLALAGRTGTRAESNLSSKQLQSDSKQNGVQDPRHRRVVTISGNSIHS 60
 DB 1 MLLIGILLITSLALAGRTGTRAESNLSSKQLQSDSKQNGVQDPRHRRVVTISGNSIHS 60
 QY 61 PKPHTYPRMVLVWRVVADEVNRIQLTDERRGLEDPPDDICKQFVVEEPPSDSVL 120
 DB 61 PKPHTYPRMVLVWRVVADEVNRIQLTDERRGLEDPPDDICKQFVVEEPPSDSVL 120
 QY 121 GRMGSGTVGKOTSKGNHRIIRFVSDYEPSEBGCIFHSIIMPQVETTSPEVLPPSS 180
 DB 121 GRMGSGTVGKOTSKGNHRIIRFVSDYEPSEBGCIFHSIIMPQVETTSPEVLPPSS 180
 QY 181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSLYKPTQLGKAFLYGKSKRVNLNL 240
 DB 181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSLYKPTQLGKAFLYGKSKRVNLNL 240
 QY 241 LKEVVKLYSCTPRNFVSITSEELKRTPTTWPGCLVYKRGNCACCLHNCNEQCVPK 300
 DB 241 LKEVVKLYSCTPRNFVSITSEELKRTPTTWPGCLVYKRGNCACCLHNCNEQCVPK 300
 QY 301 VTKKYHEVLQRPRTGVKGLKSLTDVALHEHEBCDCVCRGNAGG 345
 DB 301 VTKKYHEVLQRPRTGVKGLKSLTDVALHEHEBCDCVCRGNAGG 345
 RESULT 10
 AAY41766
 ID AAY41766 standard; protein, 345 AA.
 XX
 AC AAY41766;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO200 protein sequence.
 XX
 KM Human; PRO, EST; expressed sequence tag; PCR primer; hybridisation;
 KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KM secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN W09946281-A2.
 PN 16-SEP-1999.
 PD 08-MAR-1999; 99MO-US005028.
 PF

XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 22-MAR-1998; 98US-0079224P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 21-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 22-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 23-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083332P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 30-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0083742P.
PR 06-MAY-1998; 98US-0084466P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
DR N-PSDB; AA234236.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.
XX
PS Claim 12; Fig 207; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of CC antisense sequences. They can also be used to create transgenic animals. CC The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to CC AA41774 represent polynucleotide and polypeptide sequence given in the CC exemplification of the present invention
XX
SQ Sequence 345 AA;
Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 8, 6e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLIGLLITSLAAGRTGTRAEISNLSKLTQSSDKQNGVDDPRHRVVTISGNSIHS 60
DB 1 MSIFGLITSLAAGROGTOAESNLSKTFQSSNKGQVDDPOHERITVTGNSIHS 60
QY 61 PRPHTYPRNMYLVNRLVAVDENVRITQLFDEPRFGLEDEDDICXDFEVEBPSDGSYL 120
DB 61 PRPHTYPRNMYLVNRLVAVDENVRITQLFDEPRFGLEDEDDICXDFEVEBPSDGTIL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEYFSPBPGFCHYSITMPQVETTSPSVLPPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEYFSPBPGFCHYSITMPQVETTSPSVLPPSS 180
QY 122 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEYFSPBPGFCHYSITMPQVETTSPSVLPPSS 180
DB 122 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEYFSPBPGFCHYSITMPQVETTSPSVLPPSS 180
QY 181 LSLDLINNAVTAFSTBELIRYLEPDRKQVDDLSLYKFWQLLGAFLYGGKSKYVNL 240
DB 181 LSLDLINNAVTAFSTBELIRYLEPDRKQVDDLSLYKFWQLLGAFLYGGKSKYVNL 240
QY 241 LKEEVKLYSCPRNRSVSIIRBELKRTDITFMWGCCLVVRGCGNCCCLHNGECOCVPRK 300
DB 241 LKEEVKLYSCPRNRSVSIIRBELKRTDITFMWGCCLVVRGCGNCCCLHNGECOCVPRK 300
QY 301 VTKKHEVQLRPRKTVGKGLHSLTDVALHHEECDCVCRGNAGG 345
DB 301 VTKKHEVQLRPRKTVGKGLHSLTDVALHHEECDCVCRGSTGG 345
RESULT 11

AA30023
ID AAY30023 standard; protein; 345 AA.
XX
AC AAY30023;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human vascular endothelial growth factor related protein.
XX
KW Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
OS Homo sapiens.
XX
PN MO9937671-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US001574.
XX
PR 27-JAN-1998; 98US-007263SP.
PR 05-JUN-1998; 98US-0086089P.
PR 24-JUN-1998; 98US-0090544P.
PR 31-AUG-1998; 98US-0098548P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Dou S, Na S, Song HY;
XX
DR WPI; 1999-458680/38.
DR N-PSDB; AAX86352.
XX
PT A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding compounds.
XX
PS Claim 1; Page 56-58; 62pp; English.
XX
CC The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,
CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding
CC sequence can be used for the recombinant production of the VEGF-R protein
XX
SQ Sequence 345 AA;
Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 8,6e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLALAGORTGTRAESNLSSKQLSDPKQNGVQPRHERVTISGNGSIHS 60
Db 1 MSLLGLLLTSLALAGORTGTRAESNLSSKQLSDPKQNGVQPRHERVTISGNGSIHS 60
QY 61 PKPHTTYPNNVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEEPPSGSVL 120
Db 61 PRPHTTYPNNVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEEPPSGSVL 120
QY 121 GRMGSGGVPGKQSKGNHRIIRFVSDYFSEPEFCIHVIMVQFTFAVSPVLPPSA 180
Db 121 GRMGSGGVPGKQSKGNHRIIRFVSDYFSEPEFCIHVIMVQFTFAVSPVLPPSA 180
QY 181 LSLDLNNAVAFSTLEELIRYLEPDRMQVDLSLYKFTWOLGKAFLYGKSKYVNL 240
Db 181 LPDLNNAVAFSTLEELIRYLEPDRMQVDLSLYKFTWOLGKAFLYGKSKYVNL 240
QY 241 LKEEYKLYSCTPRNFSVIREBLKRTDTTFMPGCLLVRCGNCACCLHNCNCCQVPRK 300
Db 241 LTEEYKLYSCTPRNFSVIREBLKRTDTTFMPGCLLVRCGNCACCLHNCNCCQVPRK 300

QY 301 VTKRYHEVLTQLRPKTVGKGLHKSLLTDVALBHEHBCDVCVCRGNAGC 345
Db 301 VTKRYHEVLTQLRPKTVGKGLHKSLLTDVALBHEHBCDVCVCRGNAGC 345

RESULT 12
AAY33679
ID AAY33679 standard; protein; 345 AA.
XX
AC AAY33679;
XX
DT 11-JAN-2000 (first entry)
XX
DE Human VEGF-E protein.
XX
KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping.
XX
OS Homo sapiens.
XX
PN MO9947677-A2.
XX
PD 23-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US005190.
XX
PR 17-MAR-1998; 98US-00040220.
PR 02-NOV-1998; 98US-00184216.
XX
PA (GERTH) GENENTECH INC.
XX
PI Ferrara N, Kuo SS;
XX
DR WPI; 1999-580306/49.
DR N-PSDB; AAZ23691.
XX
PT New growth factor polypeptide useful for treating cardiovascular or
PT endothelial disorders, e.g. cardiac hypertrophy.
XX
PS Claim 1; Fig 2; 122pp; English.
XX
CC This invention describes the isolation of a novel human vascular
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
CC therapeutic, vulnery and cardiant activity. VEGF-E can be administered
CC therapeutically, especially by expressing encoding polynucleotides, to
CC treat cardiovascular or endothelial disorders in mammals, especially
CC humans. It is useful in wound repair and tissue generation and
CC regeneration, and may especially be used to treat cardiac hypertrophy. It
CC can be combined with a carrier in pharmaceutical compositions, which can
CC be administered to treat disorders as above. VEGF-E can be used to screen
CC for antagonists and agonists, and the antagonists administered to treat
CC angiogenic disorders in mammals (especially humans) e.g. cancer or age-
CC related macular degeneration. It can be used to generate antibodies, as
CC useful therapeutically as antagonists, as above. The antibodies are also
CC useful to detect VEGF-E polypeptide, especially to diagnose
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
CC vascular disease, or neovascularization associated with tumor formation),
CC by contacting the antibody with a tissue sample and detecting formation
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-
CC E can be used to diagnose cardiovascular and endothelial disorders in
CC mammals, by detecting abnormally high or low VEGF-E gene expression in
CC tissue samples. They can also be used to diagnose a disease or
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
CC detecting a mutation in the VEGF-E encoding sequence isolated from a
CC sample. They may also be used to produce probes useful to detect related
CC sequences or for gene mapping. This sequence represents the human VEGF-E
CC protein described in the method of the invention
XX
SQ Sequence 345 AA;


```

Db      1 MSFLGILLTSALAGRGQTQASNLSSKQFSSNKQNGVDPQHRRIITVSTNGSIHS 60
Qy      61 PKPHTTPRMVWLVWRLVAVDENVRIGLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
        61 PRPHTTPRMVWLVWRLVAVDENWVIGLTFDERFGLEDPEDDICKYDFVEVEEBSDSITL 120
Qy      121 GRWGSSTVGKQSKSNHRIKRVSPDEYFSEBGFCHYSIIMPOVETTSBVLPPSS 180
        121 GRWGSSTVGKQSKSNQRIKRVSPDEYFSEBGFCHIVIMPOTEAVSPVLPSPA 180
Db      121 GRWGSSTVGKQSKSNQRIKRVSPDEYFSEBGFCHIVIMPOTEAVSPVLPSPA 180
Qy      181 LSLDLNNAVTAFTLEBELRYLEPPDMQVLDLSLYKPTQQLGKAPLYGKKSRVNLNL 240
        181 LPDLNNATTAFTLEBELRYLEPPDMQVLDLSLYKPTQQLGKAPLYGKKSRVNLNL 240
Qy      241 LKEEVKLYSCTPRNFSVSIREEIKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
        241 LKEEVKLYSCTPRNFSVSIREEIKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
Qy      301 VTKKYHEVLQRPRTGVGGLHKSLLTDVALHHEBECDCVCRGNAGG 345
        301 VTKKYHEVLQRPRTGVGGLHKSLLTDVALHHEBECDCVCRGSTGG 345
Db      301 VTKKYHEVLQRPRTGVGGLHKSLLTDVALHHEBECDCVCRGSTGG 345

RESULT 14
AAB19578
ID      AAB19578 standard; protein; 345 AA.
XX
AC      AAB19578;
XX
DT      22-JAN-2001 (first entry)
XX
DE      Human PRO200 (vascular endothelial growth factor E).
XX
KW      PRO200; vascular epithelial growth factor E; VEGF-E; human;
KW      ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa;
KW      macular degeneration; retinal detachment; retinal tear; macular hole;
KW      myopia; traumatic choriorretinopathy; acute retinal necrosis syndrome;
KW      contusion; edema; retinal vision occlusion; vascular disease;
KW      retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Peptide
        1..14
        /label= Signal_peptide
        15..345
        /label= Mature_Pro200
        15..21
        /note= "N-myristoylation"
        25..29
        /note= "Asn is N-glycosylated"
        55..59
        /note= "Asn is N-glycosylated"
        117..123
        /note= "N-myristoylation"
        127..133
        /note= "N-myristoylation"
        254..258
        /note= "Asn is N-glycosylated"
        281..287
        /note= "N-myristoylation"
        282..288
        /note= "N-myristoylation"
        319..325
        /note= "Amidation"
XX
PN      WO200053760-A2.
XX
PD      14-SEP-2000.
XX
PF      10-MAR-2000; 2000WO-US006319.
XX
PR      12-MAR-1999; 99US-0123957P.

```

```

XX      (GERTH ) GENENTECH INC.
XX      Ferreira N, Goddard A, Gurney AL, Hebert C, Henzel MJ,
PI      Kabakoff RC, Klein RD, Kljavin IJ, Kuo SS, La Fleur M, Wood WI,
XX      WPI: 2000-587437/55.
DR      N-PSDB; AAB8515.
XX
PT      Novel PRO polypeptides useful for preventing or rescuing retinal cells
PT      from injury caused by ocular diseases such as retinitis pigmentosa,
PT      retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.
XX
PS      Claim 2; Fig 2; 140pp; English.
XX
CC      The present sequence is that of human PRO200 or vascular endothelial
CC      growth factor E (VEGF-E), as predicted from a cDNA clone (see AAB8515)
CC      that was isolated from a glioma cell line G61 library using probes (see
CC      AAB8523-26) based on an expressed sequence tag (see AAB8522) that
CC      showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a
CC      pI of about 6.06. A method for producing PRO polypeptides, including
CC      PRO200, using a host cell transformed with a vector comprising a PRO
CC      nucleic acid is claimed. The invention relates to the use of PRO
CC      polypeptides to delay, prevent or rescue retinal cells such as retinal
CC      neurons selected from photoreceptors, retinal ganglion cells, displaced
CC      retinal ganglion cells, amacrine cells, displaced amacrine cells,
CC      horizontal and bipolar neurons, and supportive cells (including Mueller
CC      cells and pigment epithelial cells) from injury and degradation. The
CC      retinal cells are preferably photoreceptors and photoreceptor cell injury
CC      or death is caused by retinal injury, light or environmental trauma or by
CC      an ocular disease selected from retinitis pigmentosa, macular
CC      degeneration, including age-related, retinal detachment, retinal tears,
CC      retinopathy, retinal degenerative diseases, macular holes, degenerative
CC      myopia, acute retinal necrosis syndrome, traumatic choriorretinopathies or
CC      contusion such as Purtscher's retinopathy, edema, ischemic conditions
CC      such as central or branch retinal vision occlusion, collagen vascular
CC      diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and
CC      occlusion associated with Fales disease and systemic lupus erythematosus
CC      (claimed)
XX
SQ      Sequence 345 AA;
XX
Query Match          90.2%; Score 1667; DB 3; Length 345;
Best Local Similarity 87.0%; Pred. No. 8.6e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
Qy      1 MLILGILLTSALAGRGQTQASNLSSKQLSDSKQNGVDPQHRRIITVSTNGSIHS 60
        1 MSFLGILLTSALAGRGQTQASNLSSKQFSSNKQNGVDPQHRRIITVSTNGSIHS 60
Db      61 PKPHTTPRMVWLVWRLVAVDENVRIGLTDERFGLEDPEDDICKYDFVEVEEBSDSVL 120
        61 PRPHTTPRMVWLVWRLVAVDENWVIGLTFDERFGLEDPEDDICKYDFVEVEEBSDSITL 120
Qy      121 GRWGSSTVGKQSKSNHRIKRVSPDEYFSEBGFCHYSIIMPOVETTSBVLPPSS 180
        121 GRWGSSTVGKQSKSNQRIKRVSPDEYFSEBGFCHIVIMPOTEAVSPVLPSPA 180
Db      121 GRWGSSTVGKQSKSNQRIKRVSPDEYFSEBGFCHIVIMPOTEAVSPVLPSPA 180
Qy      181 LSLDLNNAVTAFTLEBELRYLEPPDMQVLDLSLYKPTQQLGKAPLYGKKSRVNLNL 240
        181 LPDLNNATTAFTLEBELRYLEPPDMQVLDLSLYKPTQQLGKAPLYGKKSRVNLNL 240
Db      181 LPDLNNATTAFTLEBELRYLEPPDMQVLDLSLYKPTQQLGKAPLYGKKSRVNLNL 240
Qy      241 LKEEVKLYSCTPRNFSVSIREEIKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
        241 LKEEVKLYSCTPRNFSVSIREEIKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
Db      241 LKEEVKLYSCTPRNFSVSIREEIKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
Qy      301 VTKKYHEVLQRPRTGVGGLHKSLLTDVALHHEBECDCVCRGNAGG 345
        301 VTKKYHEVLQRPRTGVGGLHKSLLTDVALHHEBECDCVCRGSTGG 345
Db      301 VTKKYHEVLQRPRTGVGGLHKSLLTDVALHHEBECDCVCRGSTGG 345

RESULT 15
AAB10651

```

AA10651strandard; protein; 345 AA.
AAB10651;
19-JAN-2001 (first entry)
Human VEGF-X protein #3.
VEGF-X; vascular endothelial growth factor; human; vulnery; cyrostatic; antiinflammatory; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
Homo sapiens.
WO20037641-A2.
29-JUN-2000.
21-DEC-1999; 99WO-US030503.
22-DEC-1998; 98GB-00028377.
18-MAR-1999; 99US-0124967P.
08-NOV-1999; 99US-0164131P.
(JNANC) JANSSEN PHARM NV.
Gordon RD, Sprengel JJ, Yon JR, Dijkmans JHH, Gostewska A; Dhanaraj SM, Xu J;
WPI; 2000-442669/38.
New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds.
Claim 72; Fig 12; 127pp; English.
This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnery, cyrostatic, antiinflammatory, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein described in the method of the invention

```

Db      121 GRMGCGGTGPGKQISKNGQINIRRFVSDSEYFPSPBEGFCIHNIYVMPGPTFAVSGVLEPSSA 180
Qy      181 LSLDDLNNATVAFTSTEEILRIYLEDPRQVNDLSIYKPTWOLGKATLYGKKSKYVNNLN 240
Db      181 LPDLNNMTITAFSTIEDLIRYLEBERWQDLIEDLYRPTWOLGKAFFVFRKSRVDNLN 240
Qy      241 LKEEVLKYSTCPNPFVSIREELKPTDTIIPMGCLLYRCGNGACCELNHCNEGCVPRK 300
Db      241 LTEEVALLSCTRNPNFVSIREELKPTDTIIPMGCLLYRCGNGACCELNHCNEGCVPSK 300
Qy      301 VTKKYEHLQLRPKRTGVKGLHKSITDVALLEHHEECDCVCRGNAGC 345
Db      301 VTKKYEHLQLRPKRTGVGRGLHKSITDVALLEHHEECDCVCRSGTSG 345

Search completed: May 27, 2004, 15:44:45
Job time : 52 secs

```

Search completed: May 27, 2004, 15:44:45
Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:21 ; Search time 36.5 Seconds

(without alignments)
2982.295 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848
Sequence: 1 MLILGLLTSALAGQRTGT.....DVALEHHECDVCGRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	11	Q9QY71 mus musculu
2	1846	99.9	345	11	Q8C119 mus musculu
3	1819	98.4	345	11	Q9JHV8 Q9jvh8 mus musculu
4	1801	97.5	345	11	Q9E0X6 Q9eqx6 rattus norv
5	1667	90.2	345	4	Q9UL22 Q9ul22 homo sapien
6	1664	90.0	345	4	Q9NR11 Q9nr11 homo sapien
7	1552	84.0	345	13	Q91946 Q91946 gallus gall
8	1375	74.4	358	11	Q8K429 Q8k429 rattus norv
9	754	40.8	370	11	Q9EQP1 Q9eqp1 rattus norv
10	752	40.7	370	4	Q9GZP0 Q9gzp0 homo sapien
11	750.5	40.6	364	4	Q9BWS5 Q9bws5 homo sapien
12	746.5	40.4	370	11	Q92517 Q92517 mus musculu
13	440.5	23.8	261	11	Q8K213 Q8k213 mus musculu
14	201	10.9	923	13	Q8QF6 Q8qf6 brachydanio
15	201	10.9	923	13	Q8AXP1 Q8axp1 brachydanio
16	192.5	10.4	691	13	Q57658 Q57658 gallus gall

17	192	10.4	34	11	Q99QM4 Q99qm4 mus musculu
18	191	10.3	977	13	Q91925 Q91925 xenopus lae
19	186	10.1	735	13	Q57381 Q57381 xenopus lae
20	185	10.0	926	4	Q9U000 Q9u000 homo sapien
21	185	10.0	1015	4	Q9Y6L7 Q9y6l7 mus sapien
22	183	9.9	1012	11	Q9WV66 Q9wv66 mus musculu
23	181	9.8	241	11	Q92135 Q92135 rattus norv
24	176	9.5	609	4	Q96190 Q96190 homo sapien
25	176	9.5	644	4	Q961H5 Q961h5 homo sapien
26	176	9.5	704	4	Q9H2E1 Q9h2e1 homo sapien
27	176	9.5	923	4	Q86T59 Q86t59 homo sapien
28	175	9.5	1007	13	Q8J128 Q8j128 xenopus lae
29	174.5	9.4	3623	4	Q60494 Q60494 homo sapien
30	169	9.1	1008	13	Q9DER7 Q9der7 gallus gall
31	168	9.1	921	11	Q9QX38 Q9qx38 rattus norv
32	165	8.9	1013	11	Q62381 Q62381 mus musculu
33	165	8.9	1019	13	Q57382 Q57382 xenopus lae
34	162	8.8	1013	4	Q9N0S4 Q9n0s4 mus sapien
35	162	8.8	1013	4	Q43897 Q43897 homo sapien
36	161.5	8.7	905	13	Q800L4 Q800l4 gallus gall
37	161.5	8.7	919	13	Q8UVR0 Q8uvr0 gallus gall
38	161.5	8.7	936	13	Q8UVQ9 Q8uvq9 gallus gall
39	160	8.7	3623	11	Q70244 Q70244 rattus norv
40	158.5	8.6	145	11	Q8BP20 Q8bp20 mus musculu
41	158.5	8.6	413	13	Q7SY25 Q7sy25 brachydanio
42	158.5	8.6	926	11	Q8QZY7 Q8qzy7 mus musculu
43	158	8.5	3620	6	Q9T053 Q9t053 canis famli
44	157	8.5	276	4	Q9BRH3 Q9brh3 homo sapien
45	157	8.5	415	4	Q9UK29 Q9uk29 homo sapien

ALIGNMENTS

RESULT 1

Q9QY71 ID Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (TREMUR1.13, Created)
DT 01-MAY-2000 (TREMUR1.13, Last sequence update)
DT 01-OCT-2003 (TREMUR1.25, Last annotation update)
DE Fallolecin (Platelet-derived growth factor C).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Tsai Y.-U., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.,
RT "CDNA Cloning of fallolecin from mouse ovary."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RL binds to PDGF alpha receptor."
RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA MEDLINE=22354683; PubMed=1246851;
RX THE PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC EMBL; AF117608; AAF22516.1; -.
DR EMBL; AF266467; AAK58566.1; -.
DR

```

DR EMBL: AK033734; BAC28455.1; -.
DR EMBL: AK042767; BAC31358.1; -.
DR EMBL: AK052947; BAC35216.1; -.
DR MGD: MGI:1859631; Pdgfc.
DR GO: GO:0005576; C:extracellular; IDA.
DR GO: GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.
DR GO: GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO: GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84E82 CRC64;

Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGRTGTRASNSLSKQLSSDKQNGVDPRIHRRVTTISGNSIHS 60
   |||||
Db 1 MLLGLLLTSALAGRTGTRASNSLSKQLSSDKQNGVDPRIHRRVTTISGNSIHS 60

QY 61 PKPHTYPRNMVLWMLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSVL 120
   |||||
Db 61 PKPHTYPRNMVLWMLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180

QY 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240
   |||||
Db 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240

QY 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240
   |||||
Db 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240

QY 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
   |||||
Db 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

QY 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
   |||||
Db 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

QY 301 VTKKHEVQLRPKTVGKGLHKSITDVALHEHBECDVCGRNAG 345
   |||||
Db 301 VTKKHEVQLRPKTVGKGLHKSITDVALHEHBECDVCGRNAG 345

RESULT 2
Q8C119 PRELIMINARY; PRT; 345 AA.
ID 08C119;
AC 08C119;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor, C polypeptide.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC037696; AAH37696.1; -.
DR MGD: MGI:1859631; Pdgfc.
DR GO: GO:0005576; C:extracellular; IDA.
DR GO: GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.
DR GO: GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO: GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PD_growth_factor.

```

```

DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 99.9%; Score 1846; DB 11; Length 345;
Best Local Similarity 99.7%; Pred. No. 7.3e-166;
Matches 344; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGRTGTRASNSLSKQLSSDKQNGVDPRIHRRVTTISGNSIHS 60
   |||||
Db 1 MLLGLLLTSALAGRTGTRASNSLSKQLSSDKQNGVDPRIHRRVTTISGNSIHS 60

QY 61 PKPHTYPRNMVLWMLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSVL 120
   |||||
Db 61 PKPHTYPRNMVLWMLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFSPSGFCHYSIIMPQVETTSPSVLPPSS 180

QY 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240
   |||||
Db 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240

QY 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240
   |||||
Db 181 LSLDLNNATVAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKVNNL 240

QY 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
   |||||
Db 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

QY 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
   |||||
Db 241 LKEEVKLVSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

QY 301 VTKKHEVQLRPKTVGKGLHKSITDVALHEHBECDVCGRNAG 345
   |||||
Db 301 VTKKHEVQLRPKTVGKGLHKSITDVALHEHBECDVCGRNAG 345

RESULT 3
Q9JHVB PRELIMINARY; PRT; 345 AA.
ID Q9JHVB;
AC Q9JHVB;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse Pdgfc gene: dynamic expression in embryonic tissues during
RT organogenesis.";
RL Mech. Dev. 96:209-213 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF286725; AAF91483.1; -.
DR MGD: MGI:1859631; Pdgfc.
DR GO: GO:0005576; C:extracellular; IDA.
DR GO: GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.
DR GO: GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO: GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR SEQUENCE 345 AA; 38886 MW; FA148BBD6D362F8 CRC64;

```

Query Match 98.4%; Score 1819; DB 11; Length 345;
 Best Local Similarity 98.8%; Pred. No. 2,6e-163;
 Matches 341; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLLIGLLITLTSALAGORTGTAAESNLSSKQLQSSDKQNGVODPRHERVVTISGNGSIHS 60
 DB 1 MLLIGLLITLTSALAGORTGTAAESNLSSKQLQSSDKQNGVODPRHERVVTISGNGSIHS 60
 QY 61 PKPHTYPRMNVLMWRLVAADENRITQITPDERGLEDPEDDICKYDFVEVEEESDGSVL 120
 DB 61 PKPHTYPRMNVLMWRLVAADENRITQITPDERGLEDPEDDICKYDFVEVEEESDGSVL 120
 QY 121 GRWGSSTVGOKQSKGNHRIKRVSDPEYPSBPGFCIHYSIIMPQVETTSPSVLPSS 180
 DB 121 GRWGSSTVGOKQSKGNHRIKRVSDPEYPSBPGFCIHYSIIMPQVETTSPSVLPSS 180
 QY 181 LSLDLNNAAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAPLYGKSKRVNMLN 240
 DB 181 LSLDLNNAAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAPLYGKSKRVNMLN 240
 QY 241 LKEBVKLYSCTPRNFSVSIIBELKRTDTITPFGCLLYKRCGNCACCLHNCNCCQVPRK 300
 DB 241 LKEBVKLYSCTPRNFSVSIIBELKRTDTITPFGCLLYKRCGNCACCLHNCNCCQVPRK 300
 QY 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345
 DB 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345

RESULT 4
 Q9EOX6 PRELIMINARY; PRT; 345 AA.
 ID AC Q9EOX6; (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Spinal cord-derived growth factor.
 GN RSCDGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hister; TISSUE=Kidney;
 RX MEDLINE=21092670; Pubmed=1162582;
 RA Hamada T., U-Tei K., Imaki J., Miyata Y.;
 RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
 RT SCDF/PDGF-C/faliolefin.";
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
 RL -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AB033830; BAB19969.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; Pf00431; CUB; 1.
 DR Pfam; Pf00341; PDGF; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PSS0278; PDGF; 2; 1.
 SQ SEQUENCE 345 AA; 38734 MW; F296DA689B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 11; Length 345;
 Best Local Similarity 96.8%; Pred. No. 1.3e-161;
 Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLIGLLITLTSALAGORTGTAAESNLSSKQLQSSDKQNGVODPRHERVVTISGNGSIHS 60
 DB 1 MLLIGLLITLTSALAGORTGTAAESNLSSKQLQSSDKQNGVODPRHERVVTISGNGSIHS 60

QY 61 PKPHTYPRMNVLMWRLVAADENRITQITPDERGLEDPEDDICKYDFVEVEEESDGSVL 120
 DB 61 PKPHTYPRMNVLMWRLVAADENRITQITPDERGLEDPEDDICKYDFVEVEEESDGSVL 120
 QY 121 GRWGSSTVGOKQSKGNHRIKRVSDPEYPSBPGFCIHYSIIMPQVETTSPSVLPSS 180
 DB 121 GRWGSSTVGOKQSKGNHRIKRVSDPEYPSBPGFCIHYSIIMPQVETTSPSVLPSS 180
 QY 181 LSLDLNNAAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAPLYGKSKRVNMLN 240
 DB 181 LSLDLNNAAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAPLYGKSKRVNMLN 240
 QY 241 LKEBVKLYSCTPRNFSVSIIBELKRTDTITPFGCLLYKRCGNCACCLHNCNCCQVPRK 300
 DB 241 LKEBVKLYSCTPRNFSVSIIBELKRTDTITPFGCLLYKRCGNCACCLHNCNCCQVPRK 300
 QY 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345
 DB 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345

RESULT 5
 Q9UL22 PRELIMINARY; PRT; 345 AA.
 ID AC Q9UL22; (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Secretory growth factor-like protein FALLOLEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
 GN HSCDGF OR PDGFC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Tsai Y.-J., Lee R.K.K., Lin S.P.;
 RT "Falloleuin, a novel growth factor like gene identified in human
 RT uterus.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20317014; Pubmed=10858496;
 RA Hamada T., U-Tei K., Miyata Y.;
 RT "A novel gene derived from developing spinal cords, SCDF, is a unique
 RT member of the PDGF/VBGF family.";
 RL FEBS Lett. 475:97-102(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21347863; Pubmed=11297552;
 RA Gilbertson D.G., Duff M.B., West J.W., Kelly J.D., Sheppard P.O.,
 RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
 RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.B.;
 RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
 RT Binds to PDGF alpha and beta Receptor.";
 RL J. Biol. Chem. 276:27406-27414(2001).
 RL -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AF091434; AAF00049.1; -;
 DR EMBL; AB033831; BAB03266.1; -;
 DR EMBL; AF260738; AAK51637.1; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0008083; F:growth factor activity; TAS.
 DR GO; GO:0007417; P:central nervous system development; TAS.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; Pf00431; CUB; 1.
 DR Pfam; Pf00341; PDGF; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDB9E51F40633E78 CRC64;

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 6e-149;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRAESENLSKTLQSDSKONGVDPHREVTITSGNSIHS 60
DB 1 MSLFGLLLTSLAAGRTGTRAESENLSKTLQSDSKONGVDPHREVTITSGNSIHS 60
QY 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPDSGYL 120
DB 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPDSGYL 120
QY 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
DB 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
QY 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
DB 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
QY 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
DB 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
DB 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345
DB 301 VTKKHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345

RESULT 6

Q9NRAL PRELIMINARY; PRT; 345 AA.

ID Q9NRAL
AC Q9NRAL
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=20268201; PubMed=10806482;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uteila M.,
RA Backstrom G., Hellstrom M., Boström H., Li H., Soriano P.,
RA Bertholz C., Heidt C.-H., Alltalo K., Ostman A., Eriksson U.,
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
receptor."
RL Nat. Cell Biol. 2:302-309 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF244813; AAF80597.1; -.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CCSEA CRC64;

Query Match 90.0%; Score 1664; DB 4; Length 345;
Best Local Similarity 86.7%; Pred. No. 1.2e-148;

Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRAESENLSKTLQSDSKONGVDPHREVTITSGNSIHS 60
DB 1 MSLFGLLLTSLAAGRTGTRAESENLSKTLQSDSKONGVDPHREVTITSGNSIHS 60
QY 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPDSGYL 120
DB 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPDSGYL 120
QY 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
DB 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
QY 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
DB 121 GRWCGSGTVPKQTSKGNHRIKRFVSDEYFPPSPGFCIHYSIMPOVTTSPVLPSS 180
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLGKAFLYGKSKVYNL 240
QY 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
DB 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
DB 241 LKEEVLVSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345
DB 301 VTKKHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345

RESULT 7

Q91946 PRELIMINARY; PRT; 345 AA.

ID Q91946
AC Q91946
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white Leghorn; TISSUE=Spinal cord;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ue-Tai K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
member of the PDGF/VEGF family."
RL FEBS Lett. 475:97-102 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BAB03265.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 84.0%; Score 1552; DB 13; Length 345;
Best Local Similarity 80.3%; Pred. No. 4.5e-138;
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRAESENLSKTLQSDSKONGVDPHREVTITSGNSIHS 60
DB 1 MSLFGLLLTSLAAGRTGTRAESENLSKTLQSDSKONGVDPHREVTITSGNSIHS 60
QY 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPDSGYL 120

```

Db 61 PKPHTYPRNTVLVWRLVAVDENVMIQLTFDERFGLDEPDDICKYDFVEVEPSDGTVL 120
Qy 121 GRMGSGTVPGKQSKGNHRIIRFVSDYFSPSGFCIHSYIMPQVETTSPTVLPRSS 180
Db 121 GRMGSSSVPSRQISKGNQIRIRFVSDYFSPSGFCIHYLLVPHHTSPSSLSLPSA 180
Qy 181 LSLDLNNNAVAFSTLEBELIRYLEPDRQVLDLSLYKPTWQLGKAFLYKSKSVNLT 240
Db 181 LPLDVNNNAVAGFTVEBELIRYLEPDRQVLDLSLYKPTWQLGKAFLYKSKSVNLT 240
Qy 241 LKEEVLYSCTPRNFSVSIRESLKRDTIIPMGCLLYRGCAGCACCLANECQVPRK 300
Db 241 LKEEVLYSCTPRNFSVSIRESLKRDTIIPMLCILYRGCAGCACCHQNCQCIPTK 300
Qy 301 VTKKYHEVLQIRPKTYGKGLKSLTDVALHEHSECDCCKRNAG 345
Db 301 VTKKYHEVLQIRPKRSGVGLKSLTDVPLEHHESECDCCKNSBG 345

```

RESULT 8

```

ID 08K429 PRELIMINARY; PRT; 258 AA.
AC 08K429;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
RT Healing."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF508348; AAM47265.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;

```

Query Match 74.4%; Score 1375; DB 11; Length 258;
 Best Local Similarity 96.9%; Pred. No. 1.6e-121;
 Matches 250; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

Qy 42 QDPHERVVTISNGSIHSPKPTPTPRNVLVWRLVAVDENVRIQLTFDERFGLDEP 101
Db 1 QDPHERVVTISNGSIHSPKPTPTPRNVLVWRLVAVDENVRIQLTFDERFGLDEP 60
Qy 102 DICKYDFVEVEPSDGTVLGRMGSGTVPGKQSKGNHRIIRFVSDYFSPSGFCIHS 161
Db 61 DICKYDFVEVEPSDGTVLGRMGSGTVPGKQSKGNHRIIRFVSDYFSPSGFCIHS 120
Qy 162 IIMPQVETTSPTVLPRSSLSLDDLNNNAVAFSTLEBELIRYLEPDRQVLDLSLYKPTW 221
Db 121 IIMPQVETTSPTVLPRSSLSLDDLNNNAVAFSTLEBELIRYLEPDRQVLDLSLYKPTW 180
Qy 222 LKGAFLYGKSKSVNLTLEEVLYSCTPRNFSVSIRESLKRDTIIPMGCLLYRGC 281
Db 181 LKGAFLYGKSKSVNLTLEEVLYSCTPRNFSVSIRESLKRDTIIPMGCLLYRGC 240

```

```

Qy 282 GNCACCLANECQCVPR 299
Db 241 GNCACCLANECQCVPR 258

```

RESULT 9

```

ID 09GCT1 PRELIMINARY; PRT; 370 AA.
AC 09GCT1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tel K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDF/PDGF-C/Fallicoin."
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB052170; BAB18920.1; -.
DR PIR; JC7592; JC7592.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;

```

Query Match 40.8%; Score 754; DB 11; Length 370;
 Best Local Similarity 46.2%; Pred. No. 1.3e-62;
 Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;

```

Qy 37 EQNGVQD-PHERVVTISNGSIHSPKPTPTPRNVLVWRLVAVDENVRIQLTFDERFG 95
Db 42 ESNHLDLVLRDENIRVGTGHVQSPRPNSYPNNLLTWRLHS-QEKTRIQLAFDHQFG 100
Qy 96 LEDPEDDICKYDFVEVEPSDGS-VLGRMGSGTVPGKQSKGNHRIIRFVSDYFSPSE 153
Db 101 LEEBANDICRDEVEDVESSTVVRGRMGHKEIPRTISRTNQIKTFQSDSYVAK 160
Qy 154 PGFCIHSII--MPQ-----VTEF-----TSPSVLPSSLSLDDLNNNAVAFST 195
Db 161 PGFKTIYSPVEDPQPEAASELINMESVTSFSGVSYHSPSW-DSTLRDALDKAIAFD 219
Qy 196 LEBLIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKSVNLTLEEVLYSCTPRNF 255
Db 220 VEDLLKYFNPAWQDLENIYMDTPRYGRASY-HERSK-VDLRLNDVGRVYCTPRNH 277
Qy 256 SVSIRBELKRTDTIFWGCCLLYRGCAGCACCLANECQCVPRKTYKTYHEVLQALP- 313
Db 278 SVNIREELKLTNAVFFRCLLVORCGGCGGLTLMWRSCTSSGKTYKTYHEVLKFBPG 337
Qy 314 -KTGVKGLKSLTDVALHEHSECDCVC 339
Db 338 FKRGKAKMALVYDIQDHERCDIC 364

```

RESULT 10

```

ID 09GZP0 PRELIMINARY; PRT; 370 AA.

```

AC O9GZP0; 01-MAR-2001 (TrEMBLrel_16, Created)
AD 01-MAR-2001 (TrEMBLrel_16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel_16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel_25, Last annotation update)
DE SPINAL CORD-derived growth factor-B (MSTP036) (Iris-expressed growth
DE factor long form) (platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGFD.
OS Homo sapiens (human).
OC Bukarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN [2]
RN [3]
RN [4]
RN [5]
RN [6]
RN [7]
RN [8]
RN [9]
RN [10]
RN [11]
RN [12]
RN [13]
RN [14]
RN [15]
RN [16]
RN [17]
RN [18]
RN [19]
RN [20]
RN [21]
RN [22]
RN [23]
RN [24]
RN [25]
RN [26]
RN [27]
RN [28]
RN [29]
RN [30]
RN [31]
RN [32]
RN [33]
RN [34]
RN [35]
RN [36]
RN [37]
RN [38]
RN [39]
RN [40]
RN [41]
RN [42]
RN [43]
RN [44]
RN [45]
RN [46]
RN [47]
RN [48]
RN [49]
RN [50]
RN [51]
RN [52]
RN [53]
RN [54]
RN [55]
RN [56]
RN [57]
RN [58]
RN [59]
RN [60]
RN [61]
RN [62]
RN [63]
RN [64]
RN [65]
RN [66]
RN [67]
RN [68]
RN [69]
RN [70]
RN [71]
RN [72]
RN [73]
RN [74]
RN [75]
RN [76]
RN [77]
RN [78]
RN [79]
RN [80]
RN [81]
RN [82]
RN [83]
RN [84]
RN [85]
RN [86]
RN [87]
RN [88]
RN [89]
RN [90]
RN [91]
RN [92]
RN [93]
RN [94]
RN [95]
RN [96]
RN [97]
RN [98]
RN [99]
RN [100]
RN [101]
RN [102]
RN [103]
RN [104]
RN [105]
RN [106]
RN [107]
RN [108]
RN [109]
RN [110]
RN [111]
RN [112]
RN [113]
RN [114]
RN [115]
RN [116]
RN [117]
RN [118]
RN [119]
RN [120]
RN [121]
RN [122]
RN [123]
RN [124]
RN [125]
RN [126]
RN [127]
RN [128]
RN [129]
RN [130]
RN [131]
RN [132]
RN [133]
RN [134]
RN [135]
RN [136]
RN [137]
RN [138]
RN [139]
RN [140]
RN [141]
RN [142]
RN [143]
RN [144]
RN [145]
RN [146]
RN [147]
RN [148]
RN [149]
RN [150]
RN [151]
RN [152]
RN [153]
RN [154]
RN [155]
RN [156]
RN [157]
RN [158]
RN [159]
RN [160]
RN [161]
RN [162]
RN [163]
RN [164]
RN [165]
RN [166]
RN [167]
RN [168]
RN [169]
RN [170]
RN [171]
RN [172]
RN [173]
RN [174]
RN [175]
RN [176]
RN [177]
RN [178]
RN [179]
RN [180]
RN [181]
RN [182]
RN [183]
RN [184]
RN [185]
RN [186]
RN [187]
RN [188]
RN [189]
RN [190]
RN [191]
RN [192]
RN [193]
RN [194]
RN [195]
RN [196]
RN [197]
RN [198]
RN [199]
RN [200]
RN [201]
RN [202]
RN [203]
RN [204]
RN [205]
RN [206]
RN [207]
RN [208]
RN [209]
RN [210]
RN [211]
RN [212]
RN [213]
RN [214]
RN [215]
RN [216]
RN [217]
RN [218]
RN [219]
RN [220]
RN [221]
RN [222]
RN [223]
RN [224]
RN [225]
RN [226]
RN [227]
RN [228]
RN [229]
RN [230]
RN [231]
RN [232]
RN [233]
RN [234]
RN [235]
RN [236]
RN [237]
RN [238]
RN [239]
RN [240]
RN [241]
RN [242]
RN [243]
RN [244]
RN [245]
RN [246]
RN [247]
RN [248]
RN [249]
RN [250]
RN [251]
RN [252]
RN [253]
RN [254]
RN [255]
RN [256]
RN [257]
RN [258]
RN [259]
RN [260]
RN [261]
RN [262]
RN [263]
RN [264]
RN [265]
RN [266]
RN [267]
RN [268]
RN [269]
RN [270]
RN [271]
RN [272]
RN [273]
RN [274]
RN [275]
RN [276]
RN [277]
RN [278]
RN [279]
RN [280]
RN [281]
RN [282]
RN [283]
RN [284]
RN [285]
RN [286]
RN [287]
RN [288]
RN [289]
RN [290]
RN [291]
RN [292]
RN [293]
RN [294]
RN [295]
RN [296]
RN [297]
RN [298]
RN [299]
RN [300]
RN [301]
RN [302]
RN [303]
RN [304]
RN [305]
RN [306]
RN [307]
RN [308]
RN [309]
RN [310]
RN [311]
RN [312]
RN [313]
RN [314]
RN [315]
RN [316]
RN [317]
RN [318]
RN [319]
RN [320]
RN [321]
RN [322]
RN [323]
RN [324]
RN [325]
RN [326]
RN [327]
RN [328]
RN [329]
RN [330]
RN [331]
RN [332]
RN [333]
RN [334]
RN [335]
RN [336]
RN [337]
RN [338]
RN [339]
RN [340]
RN [341]
RN [342]
RN [343]
RN [344]
RN [345]
RN [346]
RN [347]
RN [348]
RN [349]
RN [350]
RN [351]
RN [352]
RN [353]
RN [354]
RN [355]
RN [356]
RN [357]
RN [358]
RN [359]
RN [360]
RN [361]
RN [362]
RN [363]
RN [364]
RN [365]
RN [366]
RN [367]
RN [368]
RN [369]
RN [370]
RN [371]
RN [372]
RN [373]
RN [374]
RN [375]
RN [376]
RN [377]
RN [378]
RN [379]
RN [380]
RN [381]
RN [382]
RN [383]
RN [384]
RN [385]
RN [386]
RN [387]
RN [388]
RN [389]
RN [390]
RN [391]
RN [392]
RN [393]
RN [394]
RN [395]
RN [396]
RN [397]
RN [398]
RN [399]
RN [400]
RN [401]
RN [402]
RN [403]
RN [404]
RN [405]
RN [406]
RN [407]
RN [408]
RN [409]
RN [410]
RN [411]
RN [412]
RN [413]
RN [414]
RN [415]
RN [416]
RN [417]
RN [418]
RN [419]
RN [420]
RN [421]
RN [422]
RN [423]
RN [424]
RN [425]
RN [426]
RN [427]
RN [428]
RN [429]
RN [430]
RN [431]
RN [432]
RN [433]
RN [434]
RN [435]
RN [436]
RN [437]
RN [438]
RN [439]
RN [440]
RN [441]
RN [442]
RN [443]
RN [444]
RN [445]
RN [446]
RN [447]
RN [448]
RN [449]
RN [450]
RN [451]
RN [452]
RN [453]
RN [454]
RN [455]
RN [456]
RN [457]
RN [458]
RN [459]
RN [460]
RN [461]
RN [462]
RN [463]
RN [464]
RN [465]
RN [466]
RN [467]
RN [468]
RN [469]
RN [470]
RN [471]
RN [472]
RN [473]
RN [474]
RN [475]
RN [476]
RN [477]
RN [478]
RN [479]
RN [480]
RN [481]
RN [482]
RN [483]
RN [484]
RN [485]
RN [486]
RN [487]
RN [488]
RN [489]
RN [490]
RN [491]
RN [492]
RN [493]
RN [494]
RN [495

	Matches	148;	Conservative	59;	Mismatches	92;	Indels	28;	Gaps	9
QY	37	FQNGVQD-PRHERAVTISGNGSIHSPKEPHYTPRNMLVWFLVAVDENVRIQLTDFBERFG	95							
Db	42	ESNNLTDLVYRDEDTQYKNGVQSPRPFPNYSPPNLLTLTWRLHS-QENTRIQLVFDNOFG	100							
QY	96	LEDEBDICCKDTFVEVEEPPDSGVL--GRWGSGTVPEPKTSKGNHPIRVSEYEFSE	153							
Db	101	LEAEENDICRVDPEVEDEISTSTIRGRWGKHEVPRIRSRNQIKITPKSDYFPAK	160							
QY	154	PGFCIHYSII---MPQVETFT-----SPSVLPSSSLDLNNNAVTAEST	195							
Db	161	PGFKTIYSLELDFQPAASSETNMSVSISSIGSVYNBSPVDP-TLLDALDDKIAEFDI	219							
QY	196	LEELIRVLEPDRQVQDLSLYKPTMQLGKAFLYGKSKSVNVLNLKEEVLVYSCTPENF	255							
Db	220	VEDLLKTFNPESWQEDLENNYLDTPRRRGREY-HDRSK-VDLDRINDADARYSGTPENY	277							
QY	256	SVSIRREBKRTDTTFWPEGLLVKRCGGNACCLHNCEQCQVPRKVTYKTHVUQLRP--	313							
Db	278	SVNIREBKLANVAVFFPRCLLVQRCGGCGCGGTVMNRSTCNSGKTVKYEHLVQFERGH	337							
QY	314	-KTGVGKLHSLTDVALLEHNEECPCV	339							
Db	338	IKRGGRATYALVDIQLDHNERCCIC	364							

09BWMV5	RESULT 11		
ID	PRELIMINARY;	PRT;	364 AA.
AC	09BWMV5.		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).		
GN	IEGF.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Iris;		
RA	Wistow G.;		
RT	"Iris-expressed Growth Factor (IEGF).";		
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RA	Strausberg R.;		
RL	Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AY027518; AA820082.1; -		
DR	EMBL; BC030645; AA830645.1; -		
DR	PIR; JC7591; JC7591.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0008083; F:growth factor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0005215; F:transporter activity; IEA.		
DR	GO; GO:0006810; P:transport; IEA.		
DR	InterPro; IPR000859; CUB.		
DR	InterPro; IPR000072; PD_growth_factor.		
DR	InterPro; IPR000531; TONB_boxC.		
DR	Pfam; PF00431; CUB; 1.		
DR	PROSITE; PS01180; CUB; 1.		
DR	PROSITE; PS50278; PDGF 2; 1.		
DR	PROSITE; PS00430; TONB_DEPENDENT_REC 1; 1.		
SO	SEQUENCE 364 AA; 42166 MW; 245C33EDDDE59EAC CRC64;		
Query Match	40.6%;	Score 750.5;	DB 4; Length 364;
Best Local Similarity	45.6%;	Pred. No. 2,7e-62;	
Matches 145;	Conservative 58;	Mismatches 88;	Indels 27; Gaps 8;

Oy	45	RHERVVT1SGN5HSIPKPFHTTYPYRMVLAADENVRLQTFDEPFGDEPDDIC	104		
Dd	45	RDEET1QYKGNKYVSGSPFPNYPNNLLTLTRHLS-QENTR1Q1QVNDQNGLEAEANDC	103		
Oy	105	KYDFEVEBEPDGSVYL--GRWCGSGTVPGKQTSKGNHIRIRFVSDYFEPSEPFCTIHSV1	162		
Dd	104	KYDFEVEBDS1STST1IRRCWCGHKEVPFRISRTNQIITFRSDDYFAKBPFK1YSL	163		
Oy	163	I---MPQYTET-----SPSVLPEPSSLSDLLNNAVTAFTLEELRYLE	204		
Dd	164	LEDFOPAASETMMESVTSSISGVSYNPSVTDPF-FL1DALDCKIAEPDVEEDLLKTFN	222		
Oy	205	PDRMGVUDLSLYKPFWMQGLGKAFVLYOKSKRYNNMLNKEBVLVYSGTSPNFSSTIEELK	264		
Dd	223	PEWGEDLEMMYLDTPPRYGRSY-HDRKSK-VDLDR1NDARKYSTCTPRNYSYNIREELK	280		
Oy	265	RDTTFMPFGCCLLVKRCGNCACCLLNHCNCGCVPRVTKRYKHEVLOLRP---KTVKGLH	321		
Dd	261	LANVFFPRCLLVQRCGNCGGCTYNNRBSCTCNSGTVKRYKHEVLOPFGH1KRGRAKT	340		
Oy	322	KS1TDVVALEHHEECDCVC	339		
Dd	341	MALVDIQLDHHERCDCIC	358		
RESULT 12					
ID	O92517	PRELIMINARY;	PRT, 370 AA.		
AC	O92517	OSD118;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109				
DE	Product: platelet-derived growth factor D).				
GN	Pdgfr.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BA1B/c;				
RC	MEDLINE=21231380; PubMed=11331882;				
RA	Labochaille W.J., Jeffers M., McDonald W.F., Chillaikuru R.A.,				
RA	Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,				
RA	Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,				
RA	Shinkets R.A., Rochberg J.W., Lichenstein H.S.;				
RT	"PDGF D, A Novel Protease-Activated Growth Factor.";				
RL	Nat. Cell Biol. 3:517-521(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Body;				
RA	Adechi J., Aizawa K., Akahira S., Akiura T., Arai A., Aono H.,				
RA	Arikawa T., Bono H., Catinici P., Fukuda S., Fukunishi Y., Furuno M.,				
RA	Hatsugawa T., Hara A., Hayashi N., Hizumoto K., Hirooka T., Hori F.,				
RA	Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,				
RA	Kawai J., Kojima Y., Konno H., Konda M., Koya S., Kurihara C.,				
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,				
RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,				
RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,				
RA	Tejima Y., Suzuki H., Tagami M., Tagawa A., Takahashi K., Tanaka T.,				
RA	Toyama Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,				
RA	Muramatsu M., Hayashizaki Y.;				
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Body;				
RC	MEDLINE=22354683; PubMed=12466851;				
RA	The FANTOM Consortium,				
RA	The RIKEN Genome Exploration Research Group Phase I & II Team,				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";				

RL	Nature 420:563-573 (2002).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Body;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Riken PANTOM Consortium;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690 (2001).
RN	[5]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Body;
RX	MEDLINE=99279253; PubMed=10349636;
RA	Carninci P., Hayashizaki Y.;
RT	"High-efficiency full-length cDNA cloning.";
RL	Meth. Enzymol. 303:19-44 (1999).
RN	[6]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Body;
RX	MEDLINE=20499374; PubMed=11042159;
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT	Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to
RL	prepare full-length cDNA libraries for rapid discovery of new genes.";
RN	Genome Res. 10:1617-1630 (2000).
RN	[7]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Body;
RX	MEDLINE=20530913; PubMed=11076861;
RA	Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA	Komno H., Akiyama J., Nishi K., Kitamura T., Teshiro H., Itoh M.,
RA	Sunm T., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
RA	Fujisake S., Inoue K., Ozawa Y., Izawa M., Ohara E., Matsuhiki M.,
RA	Taneda Y., Ishikawa T., Togawa K., Tanaka T., Matsura S., Kawaj J.,
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT	"RIKEN integrated sequence analysis (RISA) system-384-format
RT	sequencing pipeline with 384 multicapillary sequencer.";
RL	Genome Res. 10:1757-1771 (2000).
CC	-I SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR	EMBL; AF355583; AKK38839.1; -
DR	EMBL; AK003359; BAB32735.2; -
DR	MGI; MGI:1919035; Pdgd.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0008083; F:growth factor activity; IEA.
DR	GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR	InterPro; IPRO00859; CUB.
DR	InterPro; IPRO00072; PD_growth_factor.
DR	Pfam; PF00431; CUB; 1.
DR	SMART; SM00042; CUB; 1.
DR	SMART; SM00141; PDGF; 1.
DR	PROSITE; PS01180; CUB; 1.
DR	PROSITE; PSS0279; PDGF 2; 1.
DR	SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CXC64;
QY	Query Match
QY	Best Local Similarity 40.4%; Score 746.5; DB 11; Length 370;
QY	Matches 151; Conservative 63; Mismatches 102; Indels 31; Gaps 9;
DG	16 QRTGRAASNSISKQLQSSDKEQNGVDPFRHERVYTIGSGNSIHSPKPHPIPRMVLTVW 75
DG	26 QRASIKALRNAN---LRRDSNMHTLDYOEEINIQVTSNHVSPPREPNPLLLTW 81
DG	76 RLVAIVDEVRVQLTFDFERFGLDEPDDICRYDFVEVERPSGS--VLGRMGCSGVPGKO 133
DG	82 WLRS-QEKTRIQLSFDHQFGLEENBDICRYDFVEVEVSSSYTVRGKRGCHKEIPRI 140
DG	134 TSKGNHIRIRFVSDPEPSPFCFIHSII--MPVTEIT-----SPSV 175
DG	141 TSRNQKITFTKSDDYFAFKGCFITYSFVEDPQPEAASETNWESVTSFSFGSVYHSPSI 200
DG	176 LPSSSLISDLINNAVTAFTSEELIRLYEPFRQVDDLSLYKPWMOLGKAFLYGKSKV 235
DG	201 TDP-TLTADADAKTVAEDTYEDDKLNPNVSWODDENLVLDTPHYHGSRV-HDRSK- 257

QY 236 UNINLKEEVKLYSCPTPRNFSVSI REBELKRTDTI FMPGCLVYKRCGNCACCLHNCCEQ 295
 Db 258 VDLDRINDVDYKRSYSCPTPRNHSVNLREBLKLTNAVFPPRCILVQRCGNCGCGTVMKSC 317
 QY 296 CVRKATYKTKHVELYQLR--KTVGKGLHSLDVALHNEEDCCVC 339
 Db 318 CSSGKTVKKYHVELKPEPHFKRGRKAKMALVYDIQDHERDCIC 364

RESULT 13

Q8K2L3 PRELIMINARY; PRT; 261 AA.
 AC Q8K2L3;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Similar to platelet-derived growth factor, D polypeptide.
 GN PDGFD.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL: BC030896; AAH30896.1; -.
 DR MGI: 1919035; Pdgfd.
 DR InterPro: IPR000859; CUB.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR PROSITE: PS01180; CUB; 1.
 SQ SEQUENCE 261 AA; 30228 MW; 2EECF6373A52D09 CRC64;

Query Match 23.8%; Score 440.5; DB 11; Length 261;
 Best Local Similarity 38.7%; Pred. No. 3.4e-33;
 Matches 94; Conservative 49; Mismatches 73; Indels 27; Gaps 7;

QY 16 ORGTAEASNLSSKQLQSDPKQNGVDPHREAVTISGSGSHSPKPHTYRNMVW 75
 Db 26 QRSIALRKVAN---LRRESNHLTDLYREBNIOVTSNGHVQSPFPSPYRNLLTW 81
 QY 76 RLVAVDENVRIQLTDFERFGLDEPDDICKYDFEVEEPPSDG--VLGRWCGSGTVPKQ 133
 Db 82 WLRS-QEKTRIQSLFPHQGLLEAENDICRYDFVEVEBVSSESTVVRGRKCHKEIPRI 140
 QY 134 TSKGNHRIIRFVSDYFPSEPGFCIHYSIT--MPOVTEFT-----SPSV 175
 Db 141 TSTRNQIKITFKSDDYFAKPGFKIYYSFVEDSQPAASETNWESYTSSPFGVSHSPSI 200
 QY 176 LRPSSLSLNLNNAVAFSTLEELIYVLEPDQVUVDLSYKPTWLLGAFIYGGKSY 235
 Db 201 TDP-TLTAADLDKTVAFPTVEDLKGHFVSWODLENLVYDTPHYRGSY-HDRKSG 258

QY 236 VNL 238
 Db 259 IEV 261

RESULT 14

Q8QFX6 PRELIMINARY; PRT; 923 AA.

AC Q8QFX6;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Neupolin-1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]
 RP SEQUENCE FROM N.A.

RA Lee P., Golish K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
 RT "Neupolin-1 is required for normal vascular development and is a
 mediator of VEGF-dependent angiogenesis in zebrafish."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.

CC EMBL: AY064213; AAL40862.1; -.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0004872; P:receptor activity; IEA.

DR GO: GO:0007155; P:cell adhesion; IEA.

DR InterPro: IPR000859; CUB.

DR InterPro: IPR000421; FAS8_C.

DR InterPro: IPR008979; Gal_Bind_1like.

DR InterPro: IPR000998; MAM_domain.

DR Pfam: PF00431; CUB; 2.

DR Pfam: PF00754; F5_F8_type_C; 2.

DR Pfam: PF00629; MAM; 1.

DR SMART: SM00042; CUB; 2.

DR SMART: SM00231; FAS8C; 2.

DR SMART: SM00137; MAM; 1.

DR PROSITE: PS01180; CUB; 2.

DR PROSITE: PS01285; FAS8C_1; 1.

DR PROSITE: PS01286; FAS8C_2; 2.

DR PROSITE: PS50022; FAS8C_3; 2.

DR PROSITE: PS00740; MAM_1; 1.

DR PROSITE: PS50060; MAM_2; 1.

DR GlycoProtein; Receptor; Transmembrane.

KW SEQUENCE 923 AA; 102492 MW; 2ED84B129AA97B2D CRC64;

Query Match 10.9%; Score 201; DB 13; Length 923;
 Best Local Similarity 27.9%; Pred. No. 8.3e-10;
 Matches 63; Conservative 31; Mismatches 74; Indels 58; Gaps 10;

QY 1 MILLGLLTLTSLAQRCTGTRAEASNLSSKQLQSDPKQNGVDPHREAVTISGSGSHS 60
 Db 8 ILFTGLTIVLSALKNDKCCDN-----IRITSANYLTS 39
 QY 61 PKRPHYPRNMVNLVAVDENVRIQLTDFERFGLDEPDDICKYDFEVEEPPSD--GS 118
 Db 40 PGKPSYYSQCIWITAPGNQRLINFNHFDLEDE---CKYDYEVAVDGVDENG 96
 QY 119 VLGRWCGSGTVPKQTSKGNHRIIRFVSDYFPSEPGFCIHYSIT--PQVTE--TSPS 174
 Db 97 LVGKYCGK-IAPSPVSSGNQLFIKIVSD-YETHGAGFISRIYEIFKTGPCEGRNFTSSSG 154
 QY 175 VLP-----PSLSLDL-----LNNAVTAFSTLEELIYVLEPD 206
 Db 155 VIKSGPPEKYPNNLDCTFMIPAKMSEIVLEFSEFE-----LEPD 195

RESULT 15

Q8AXP1 PRELIMINARY; PRT; 923 AA.

AC Q8AXP1;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Neupolin-1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Shoji W., Tawarayama H.;

RT "The cloning and expression of neuropilin-1."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB088776; BAC53657.1; -
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000421; FA58 C.
 DR InterPro: IPR008979; Gal Bind like.
 DR InterPro: IPR000998; MAM_domain.
 DR Pfam: PF00431; CUB; 2.
 DR Pfam: PF00754; F5_F8_type_C; 2.
 DR Pfam: PF00629; MAM; 1.
 DR SMART: SM00042; CUB; 2.
 DR SMART: SM00231; FA58C; 2.
 DR SMART: SM00137; MAM; 1.
 DR PROSITE: PS01180; CUB; 2.
 DR PROSITE: PS01285; FA58C_1; 1.
 DR PROSITE: PS01286; FA58C_2; 2.
 DR PROSITE: PS50022; FA58C_3; 2.
 DR PROSITE: PS00740; MAM_1; 1.
 DR PROSITE: PS50060; MAM_2; 1.
 SQ SEQUENCE 923 AA; 102541 MW; 0B6CE33ED28A21F7 CRC64;

Query Match 10.9%; Score 201; DB 13; Length 923;
 Best Local Similarity 27.9%; Pred. No. 8.3e-10;
 Matches 63; Conservative 31; Mismatches 74; Indels 58; Gaps 10;

QY 1 MLLIGLLILTSALAGQRTGTAESNLSSKLQSSDPKEQNGVQDPRHRYVTISGNGSIHS 60
 DB 8 ILFTGIFLIVSALNDRKCGDN-----IRITSANYLYTS 39
 QY 61 PKPHTYPRNNVLVRLVAVDENVRIQLFDERFGLDEPDDICKYDFVEVEBPSD--GS 118
 DB 40 FGIVSYTPSOKCIWVITAPGNORILINFNPHFDLEDRE--CKNDYVEVRDGVDENGQ 96
 QY 119 VLGRWCGSGTVPGKQTSKGNHRIKRVSDERYPSSEPGFCIHYSIIM--PQYTE--TTSPS 174
 DB 97 LVGKYCGK-IAPSPVSSGNGLFIKFVSD-YETHGAGFSIRYEIFKIGPECSRNPSTSSG 154
 QY 175 VLP-----PSSLISLDL-----LNNAVTAFSTLEELIRYLEPD 206
 DB 155 VIKSPGPEPEKYPNNIDCTFMIFAPMSRIVLEFESFE-----LEPD 195

Search completed: May 27, 2004, 15:46:43
 Job time : 37.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:56 ; Search time 14 Seconds
(without alignments)
2370.434 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLGLLLSALAGQRTGT.....DVALEHHECDVCVCRNAGG 345

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	754	40.8	370	2	JC7592
2	753	40.7	370	2	JC7591
3	746.5	40.4	370	2	JC7998
4	191	10.3	707	2	JC2218
5	190	10.3	823	1	A58788
6	183.5	9.9	730	1	BMH41
7	183.5	9.9	927	1	J00948
8	181	9.8	986	1	B58788
9	181	9.8	986	1	B58788
10	174.5	9.4	3623	2	T09456
11	160	8.7	3623	2	T08618
12	158	8.5	449	2	A55362
13	153	8.3	1057	1	A59288
14	147.5	8.0	1524	2	T30337
15	145.5	7.9	686	1	A59271
16	144	7.8	699	1	I54763
17	143.5	7.8	597	2	S71352
18	141.5	7.7	1070	2	T31069
19	140.5	7.6	3871	2	T22812
20	139	7.5	1594	2	T30549
21	137.5	7.4	705	1	C1HURB
22	135.5	7.3	1464	2	S58984
23	133.5	7.2	402	2	JH0403
24	128	6.9	277	2	A41735
25	127	6.9	419	2	S69207
26	126.5	6.8	579	2	JC7629
27	125.5	6.8	245	1	TVCTSS
28	125.5	6.8	767	2	T30018
29	125	6.8	533	2	JC7985

30	123	6.7	275	2	JC6506	tumor necrosis fac
31	122.5	6.6	2403	2	A59386	sanko - human
32	119.5	6.5	2083	2	T42721	CRP-ductin-alpha p
33	117.5	6.4	276	2	A47290	TSG-6 homolog PS4
34	117.5	6.4	1290	2	A57190	ebnerin precursor
35	114.5	6.2	200	2	I51551	platelet-derived g
36	114.5	6.2	215	2	S08220	platelet-derived g
37	114.5	6.2	226	2	I51550	platelet-derived g
38	113	6.1	695	1	S05008	complement subcomp
39	112.5	6.1	241	1	PFH052	platelet-derived g
40	111.5	6.0	226	1	TFMVSS	PDGF-related trans
41	109	5.9	694	2	JC6554	complement subcomp
42	108.5	5.9	148	2	D49530	16K vascular endot
43	107	5.8	321	2	T33161	hypothetical prote
44	104	5.6	319	2	I51569	UVS.2 protein - Af
45	103.5	5.6	225	2	S25097	platelet-derived g

ALIGNMENTS

RESULT 1

spinal cord-derived growth factor-B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C:Accession: JC7592
R/Hamada, T.; Oi-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Contents: Fetal brain
A:Accession: JC7592
A:Molecule type: mRNA
A:Residues: 1-370 <HAM>
A:Cross-references: DDBJ:AB052170
C:Genetics:
A:Gene: scdGF-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gro
F:294-308/Region: conserved motif #status predicted

Query Match	Score	DB 2:	Length	370:
Best Local Similarity	46.2%	Pred. No. 1.4e-55;		
Matches 151;	Conservative 62;	Mismatches 86;	Indels 28;	Gaps 10;
QY	37	EONGVOD-PHERVVTISGSGSIHSPKPTPRNVLVRLVAVDENVRIQLFEDRFQ 95		
DB	42	ESNHLTDLVRRDENIRVTGTGHVQSPFPNSYPNNLLTWRLHS-QEKTRIQLAFDHFG 100		
QY	96	LEDEDDICRYDFEVEVERPSDGS--VLGRNCGSGTGVGKOTSKGNHRIKRVFSDEYPSPE 153		
DB	101	LEBAENDICRYDFEVEVDVSESSITVGRNCGKHEIPRTSRNOKIKIFQSDIYVAK 160		
QY	154	PGFCIHYSIT--MPQ-----VTET-----TSPSYLPPSSSLDLINNAVTAFT 195		
DB	161	PGFVIYVSFVEDQPEAASEINNESVTSFSGVSYHPSVM-DSTLADALDKAIAFDFT 219		
QY	196	LEELIRYLEPDRNOVDLSLYKPTWOLGKAFYLGKSKVYNLNLKEBYKLVSCPRNF 255		
DB	220	VEDLLKTFNPASWODDLENIYMDTPRYGRSY-HERSK-VLDRLNDVRYSCPRNH 277		
QY	256	SVSIRBELKRTDTIFMPGCLLVKRCGNCACCLHNCEQCVPRKTVKKHVEVQLARP-- 313		
DB	278	SVNIREELKLTNAVFFPRCLLVORCGNCCCGTLNWKSCITCSGKTVKKHVEVQLARP 337		
QY	314	KTVGKGLHSLTDVALEHHECDVCVC 339		
DB	338	FKRRGKAKMALVDIQDHHERCDCIC 364		

N:Alternate names: bone morphogenic protein splice form BMP-1/His
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; A58788
R:Moroney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EKRPALOPRGRHOLKFRYQKRRTPQ' <WQ2>
A:Cross-references: GB:M22488; NID:g179499; PIDN:AA51833.1; PID:g179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 33572-33578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (mtld) are encod
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TK>
A:Cross-references: GB:L35278; NID:g619423; PIDN:MAC41703.1; PID:g619424
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g
F:1-22/Domains: signal sequence #status predicted <SIG>
F:23-823/Product: procollagen C-endopeptidase splice form His #status predicted <MAT>
F:130-321/Domains: astacin homology <AST>
F:322-431/Domains: C1r/C1s repeat homology <C1R1>
F:435-544/Domains: C1r/C1s repeat homology <C1R2>
F:551-587/Domains: EGF homology <EGF>
F:591-700/Domains: C1r/C1s repeat homology <C1R3>
F:738-752/Region: histidine-rich
F:911,142,333,363,559/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,372/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match	Local Similarity	Score 190;	DB 1;	Length 823;
Beat	Local Similarity	36.0%;	Pred. No. 9.9e-08;	
Matches	54; Conservative	20; Mismatches	48; Indels	28; Gaps 7;

QY	55	NGSISKRPETHPTNNMVLWRILVADENVRIQLTFDRFGLEDDEDICTDYVEVEE	113
DB	599	NGSISPCWPKPEYPPNKNCIQVLVAPTO-YRISLSFD--PFEEGNDVCKYDFEVRSG	654
QY	114	-PSDSVLGRMGCGSTGVGKQTSKGNHRIKRFVSDPEFPSPGCTHY-----	160
DB	655	LTADSKLHGKRCGS-EKREVITTSQYNNKRVKFSKDNVY-SKKGFAPFVSLGAGDRHS	712
QY	161	-----SIIMPOVTEETSSPSVLPSSLSLD	184
DB	713	HLSGELLLCPHALVDVTVA--PPEALHGD	740

RESULT 6
BMMU1
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
N:Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: A37278; B58788
R:Moroney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-730 <WQ2>

[illegible]

Db 1 ITTSPSYLTASGVPHSPYSGQRCEMLIQAPEHYQININPHHDLBRE---CKYD V 87
 Oy 110 EV--EPPSDGSVIGRWGSGTVPCKQTSKGNHIRIRFVSDEYFSPGFCIHYSTM-P 165
 Db 88 EVIDGNANGQLLKGYCGK-IAPSPLVSTGPSIFIRFVSDEYTPG-AGFSIYEVFKTGP 145
 Oy 166 QVTE--TTSPSVLP-----PSSLIDLNNVNTARSTEEILRLRYEPDRMOVDLS 214
 Db 146 ECSRNTSSNGVKSPPYKPKYPALECTYIIFA----PKQEIY--LEFSEFLPADS 198
 RESULT 8
 B58788
 Procollagen C-endopeptidase (EC 3.4.24.19) precursor, collagen-like splice form - human
 C.Alternate names: bone morphogenic protein 1, collagen-like splice form
 C.Species: Homo sapiens (man)
 C.Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
 C.Accession: A37278; B58788
 R.Wozney, J.M.; Rosen, V.; Celeste, A.J.; Matsuoka, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1998
 A.Title: Novel regulators of bone formation: molecular clones and activities.
 A.Reference number: A37278; PMID:89072730; PMID:3201241
 A.Accession: A37278
 A.Molecule type: mRNA
 A.Residues: 1-702; 'EKRPALQPPRGPHQLKFRVQRKRRTPQ' <NOZ>
 A.Cross-references: GB:U2488; NID:G179499; PIDN:AAA51833.1; PID:G179500
 R.Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A.Title: Bone morphogenetic protein-1 and a mammalian collagen homologue (mtId) are encoded
 A.Reference number: A58788; PMID:95096114; PMID:798260
 A.Accession: B58788
 A.Molecule type: mRNA
 A.Residues: 703-986 <TAK>
 A.Cross-references: GB:U35279; NID:G619860; PIDN:AAC41710.1; PID:G619861
 C.Genetics:
 A.Gene: GDB:BMP1; BMP-1
 A.Cross-references: GDB:125203; OMIM:112264
 A.Map position: 8p21-8p21
 C.Function:
 A.Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 A.Descriptfamily: procollagen C-endopeptidase; aspartic homology; C1r/C1s repeat homology; B
 C.Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g
 F.1-22/Domain: signal sequence #status predicted <Sig>
 F.123-986/Product: procollagen C-endopeptidase collagen-like splice form #status predicted
 F.130-331/Domain: aspartic homology <AST>
 F.322-431/Domain: C1r/C1s repeat homology <C1R1>
 F.435-544/Domain: C1r/C1s repeat homology <C1R2>
 F.551-587/Domain: EGF homology <EG1>
 F.591-700/Domain: C1r/C1s repeat homology <C1R3>
 F.707-742/Domain: EGF homology <EG2>
 F.747-856/Domain: C1r/C1s repeat homology <C1R4>
 F.860-973/Domain: C1r/C1s repeat homology <C1R5>
 F.912-142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F.213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F.214/Active site: Glu #status predicted
 F.565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 Query Match 9.8%; Score 181; DB 1; Length 986;
 Best Local Similarity 42.6%; Pred. No. 7, 1e-07;
 Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
 Oy 55 NSGISPKFPHYPRNNVTVLRVAVDENVRILQTFDERFGLEDDEDDICKYFVVEE- 113
 Db 539 NSISITPGWPKPEKPPNKNCIWOLVAPTO-XRISIQFD--PFETGNDVCKYDFVBSG 654
 Oy 114 -PSDGSVLRMGSGGVTPGKQTSKGNHIRIRFVSDEYFSPGFCIHY 160
 Db 655 LTRDSKLGKFCGS-EKPEVITSTQYNNRVEFKSDNTV-SKKGFAHF 700
 RESULT 9

149540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: 149540
R:Fukagawa, M.; Nobori, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A>Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is re
A:Reference number: 149540; MUID:94229342; PMID:8174772
A:Accession: 149540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: GB:I24755; NID:g439606; PIDN:AAA3306.1; PID:g439607
C:Genetics:
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; h
C:Keywords: hydrolase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EGF>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted

```

Query March 9.8%; Score 181; DB 2; Length 991;
Best Local Similarity 42.6%; Pred. No. 7.2e-07;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

QY 55 NGSIHSKFPHTYPRNNVWLVRILVAVDENVRIQLTPDERFGLBDEDDICKYDFVEVEE-113
DB 604 NGSIITSGWMPREYPPNKGCIWQLVAPQ-QYRISLQF---FFETBEGNDVCKYDFVEVRSG 659
QY 114 -PSGASVLRKRCGSGVTPGKOTSKGNHRRFVSDEFPSBPQCITY 160
DB 660 LTTADSKLHGKFCGS-EKPEVITSGYNNMRVEFSKDNIV-SKKGKAF 705

RESULT 10
T09456
Intrinsic factor-B12 receptor Cubilin precursor - human
C|Species: Homo sapiens (man)
C|Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C|Accession: T09456
R|Koyzaki, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A|Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteri-
ion.
A|Reference number: Z16677; MUID:98241400; PMID:9572993
A|Accession: T09456
A|Status: preliminary; translated from GS/EMBL/DBD
A|Molecule type: mRNA
A|Residues: 1-3623 <KOZ>
A|Cross-references: EMBL:AF034611; NID:G9329528; PIDN:ACG82612.1; PID:G9329529
C|Genetics:
A|Map position: 10P12
C|Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C|Keywords: receptor; vitamin B12 uptake
F|1-24/Domain: signal sequence #status predicted <SIG>
F|25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F|436-467/Domain: EGF homology <EGF>

Query March 9.4%; Score 174.5; DB 2; Length 3623;
Best Local Similarity 31.9%; Pred. No. 1.3e-05;
Matches 53; Conservative 26; Mismatches 64; Indels 23; Gaps 8;

QY 15 GORTGTRAESNLISK-----LQLSSD--KEONGVDRHRHVVTISGNSIH-----59
DB 2173 GHFGSGAASLTFTSDNQMFVQFISDHSNNGGFKRYEAKSLACGSNVYIHDADSAGY 2222
QY 60 -SPKPHPTYPNNVWLVRILVAVDENVRIQLTPDERFGLBDEDDICKYDFVEVEE--PSD 116
DB 2233 TSPHNPNNYPHADCCITLAPPE-TRIQGFQFERFPIETVPPN--CTSNVLEADGVSD 2289

```


QY 127 GTVPGKQTSKGNHRIKRVSD 147
 | : : : : :
 Db 547 KLPENIKT-RSNQMVFIRFVSD 566

RESULT 14

T30337

polyprotein - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003

C/Accession: T30337

R/Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.

Submitted to the EMBL Data Library, March 1998

A/Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from Xé

A/Reference number: Z20829

A/Accession: T30337

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1524 <YAN>

A/Cross-references: EMBL:U01290; NID:G2981640; PID:G2981641; PIDN:AAC24717.1

C/Superfamily: tyrosin related polypeptide; trypsin homology

Query Match 8.0%; Score 147.5; DB 2; Length 1524;
 Best Local Similarity 28.7%; Pred. No. 0.00082;
 Matches 54; Conservative 34; Mismatches 73; Indels 27; Gaps 10;QY 56 GSIIHSPKPHPTYPNNVLRVAVDENVRIOITFDERFGLDEPDIDCKYDFVEV-EEP 114
 | : : : : :
 Db 439 GMIISEPPYPRPPKLTCSN-ITLAPENHIVKLFED-FNVEYGHG--CIYDAVEYDGA 494QY 115 SDGSVLGRWCGSGTVPKQTSKGNHRIKRVSDYFPPSEPGFCIHYSIIMPO-----VT 168
 | : : : : :
 Db 495 EEKQLIARLQGY-TLPPISSPENTMIRFKTD-MENSYPGFKKSFVPEKEQFSLPVD 552QY 169 ETTSPSVLPSSSLDILNNA-VTAFSTLEELIRYIEPD---RMQYDL-----DS 214
 | : : : : :
 Db 553 DTFPIISMILHRAIALDVCGMAPTPKWMLPRIVGGEASPNMSPWQVIFFLRTFHCEGA 612QY 215 LYEPTWQL 222
 | : : : : :
 Db 613 IISPPWTL 620

RESULT 15

A59271

Ra-reactive factor (EC 3.4.21.-) 2 precursor - human

N/Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)

C/Species: Homo sapiens (man)

C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000

C/Accession: A59271

R/Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, K.

Nature 386, 506-510, 1997

A/Title: A second serine protease associated with mannan-binding lectin that activates c

A/Reference number: A59271; MUID:97242412; PMID:9087411

A/Accession: A59271

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-686 <JEN>

A/Cross-references: NID:G4007626; PIDN:CAA71059.1; PID:G4007627

A/Experimental source: GB:Y09926; PIDN:CAA71059.1; PID:G4007627

A/Note: submitted to GenBank, December 1996

C/Note: parts of this sequence, including the amino end of the mature protein, were dete

C/Genetics:

A/Gene: GDB:MASP2

A/Cross-references: GDB:6071500

A/Map position: 1p36.2-1p36.3

C/Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H

C/Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine P

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-44/445-686/Product: Ra-reactive factor 2 #status predicted <MAT>

F/19-134/Domain: C1r/C1s repeat homology <C1R1>

F/142-180/Domain: EGF homology <EGF>

F/184-293/Domain: C1r/C1s repeat homology <C1R2>
 F/300-361/Domain: complement factor H repeat homology <FH1>
 F/366-430/Domain: complement factor H repeat homology <FH2>
 F/445-679/Domain: trypsin homology <TRY>
 F/72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552
 F/158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F/444-445/Cleavage site: Arg-116 (autolytic) #status predicted
 F/483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 7.9%; Score 145.5; DB 1; Length 686;

Best Local Similarity 30.8%; Pred. No. 0.00043;

Matches 33; Conservative 27; Mismatches 42; Indels 5; Gaps 4;

QY 55 GSIIHSPKPHPTYPNNVLRVAVDENVRIOITFDERFGLDEPDIDCKYDFVEV-EEP 114
 | : : : : :
 Db 193 SGEISPPYPRPPKLTCSN-ITLAPENHIVKLFED-FNVEYGHG--CIYDAVEYDGA 494QY 115 SDGSVLGRWCGSGTVPKQTSKGNHRIKRVSDYFPPSEPGFCIHYSIIMPO-----VT 161
 | : : : : :
 Db 250 TDREHGPFCGK-TLPRIETKSNVTITFVDE-SGDHTGWKIHYT 294

Search completed: May 27, 2004, 15:47:23
 Job time : 15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:38:06 ; Search time 10.5 Seconds
(without alignments)
1710.877 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
Sequence: 1 MLILGLLTLTSLALAGRTG.....DVALLHHHGGDCVCGRNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	10.3	707	1	BMP1_XENLA
2	183.5	9.9	928	1	NPRI_XENLA
3	181	9.8	986	1	BMP1_HUMAN
4	181	9.8	991	1	BMP1_MOUSE
5	176	9.5	923	1	NPRI_HUMAN
6	174	9.4	1022	1	TID_BRAR
7	172	9.3	922	1	NPRI_RAT
8	169	9.1	923	1	NPRI_MOUSE
9	167	9.0	914	1	NPRI_CHICK
10	163.5	8.8	616	1	SPAN_STRPU
11	158	8.5	449	1	PCOI_HUMAN
12	155.5	8.4	925	1	NPRI_RAT
13	155.5	8.4	931	1	NPRI_MOUSE
14	155.5	8.4	931	1	NPRI_MOUSE
15	153.5	8.3	326	1	VEGD_RAT
16	153	8.3	1057	1	TID_DROME
17	147.5	8.0	704	1	CRAR_MOUSE
18	145.5	7.9	686	1	MAS2_HUMAN
19	145.5	7.9	3565	1	CSM1_HUMAN
20	144.5	7.8	597	1	BP10_PARLI
21	144	7.8	699	1	CRAR_HUMAN
22	137.5	7.4	705	1	CIR_HUMAN
23	136.5	7.4	468	1	PCOI_RAT
24	136	7.4	354	1	VEGD_HUMAN
25	135.5	7.3	358	1	VEGD_MOUSE
26	133.5	7.2	468	1	PCOI_MOUSE
27	132	7.1	415	1	VEGD_MOUSE
28	131.5	7.1	3564	1	CSM1_MOUSE
29	130	7.0	639	1	BMP1_STRPU
30	128	6.9	277	1	TS6G_HUMAN
31	127	6.9	419	1	VEGD_HUMAN
32	125.5	6.8	245	1	PDGB_FELCA
33	124.5	6.7	3670	1	CSM3_HUMAN

34	123	6.7	275	1	TS6G_MOUSE
35	119.5	6.5	3487	1	CSM2_HUMAN
36	117.5	6.4	276	1	TS6G_RABIT
37	114.5	6.2	226	1	PDGA_XENLA
38	113	6.1	695	1	CASP_MESAU
39	112.5	6.1	241	1	PDGB_HUMAN
40	111.5	6.0	164	1	VEGA_CAVPO
41	111.5	6.0	226	1	TS1S_SMSAV
42	109	5.9	855	1	ST14_HUMAN
43	108.5	5.9	148	1	VEGH_ORPN7
44	108	5.8	2796	1	CSM3_MOUSE
45	105.5	5.7	207	1	VEGB_HUMAN

ALIGNMENTS

RESULT 1	ID	BMP1_XENLA	STANDARD;	PRT;	707 AA.
AC	P98070;	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).				
OS	Xenopus laevis (African clawed frog).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;				
CC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Embryo; PubMed=8262384;				
RX	MEDLINE=94085787; PubMed=8262384;				
RA	Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;				
RT	"Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein-1 during early embryonic development.";				
RT	Gene 134:257-261 (1993).				
RL	Gene 134:257-261 (1993).				
CC	-1- FUNCTION: Involved in pattern formation in gastrula and later differentiation of developing organs.				
CC	-1- DEVELOPMENTAL STAGE: Blastula, early gastrula and hatched tadpoles; little or no expression in morula and late gastrula.				
CC	-1- SIMILARITY: Belongs to peptidase family M12A.				
CC	-1- SIMILARITY: Contains 1 EGF-like domain.				
CC	-1- SIMILARITY: Contains 3 CUB domains.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; L12249; AAA16313.1; -				
DR	PIR; JC2218; JC2218.				
DR	HSSP; P00736; IAPQ.				
DR	MEROPS; M12.005; -				
DR	InterPro; IPR000152; Asx_hydroxyl_S.				
DR	InterPro; IPR000859; CUB.				
DR	InterPro; IPR001881; EGF_Ca.				
DR	InterPro; IPR006209; EGF_Like.				
DR	InterPro; IPR006025; Pept_M_zn_BS.				
DR	InterPro; IPR006026; Peptidase_M.				
DR	InterPro; IPR001506; Peptidase_M12A.				
DR	Pfam; PF01400; Astacin; 1.				
DR	Pfam; PF00431; CUB; 3.				
DR	Pfam; PF00008; EGF; 1.				
DR	PRINTS; PR00480; ASTACTIN.				
DR	SMART; SM00042; CUB; 3.				
DR	SMART; SM00179; EGF_Ca; 1.				
DR	SMART; SM00235; ZnMC; 1.				
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.				

Db 146 ECSNFTSSNGVSKPKYPERYALNLECTYIIFA----PKMQEIV--LEPESFELEADS 198

RESULT 3

BMP1_HUMAN STANDARD; PRT; 986 AA.

AC P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;

DT 01-JAN-1990 (Rel. 13, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)

DS (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (MT1d).

GN BMP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

PN [1]

RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).

RC TISSUE=Skin;

RX MEDLINE=96209868; PubMed=8643539;

RA Li S.W., Sieron A.L., Ferrala A., Hojima Y., Arnold W.V., Prockop D.J.;

RT "The C-proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic protein-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).

RX MEDLINE=89072730; PubMed=3201241;

RA Wozney J.M., Rosen V., Celeste A.J., Mittleman B., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.;

RT "Novel regulators of bone formation: molecular clones and activities.";

RL Science 242:1528-1534(1988).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).

RC TISSUE=Placenta;

RX MEDLINE=96160316; PubMed=9500680;

RA Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;

RT "Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1.";

RL J. Mol. Med. 76:141-146(1998).

RN [4]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).

RC TISSUE=Placenta;

RX MEDLINE=95096114; PubMed=7798260;

RA Takahara K., Lyons G.E., Greenspan D.S.;

RT "Bone morphogenetic protein-1 and a mammalian tolloid homologue (MT1d) are encoded by alternatively spliced transcripts which are differentially expressed in some tissues.";

RL J. Biol. Chem. 269:32572-32578(1994).

RN [5]

RP DISULFIDE BOND IN METALLOPROTEASE DOMAIN.

RX MEDLINE=21336528; PubMed=11263002;

RA Garrigue-Ancar L., Barker C., Kadler K.E.;

RT "Identification of amino acid residues in bone morphogenetic protein-1 important for procollagen C-proteinase activity.";

RL J. Biol. Chem. 276:26237-26242(2001).

CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II and III. Induces cartilage and bone formation.

CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type III.

CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-endopeptidase enhancer protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=7;

CC Name=BMP1-3;

CC IsoId=P13497-1; Sequence=Displayed;

CC Name=BMP1-1;

CC IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;

CC Name=BMP1-2;

CC IsoId=P13497-7; Sequence=Not described;

CC Name=BMP1-4;

CC IsoId=P13497-3; Sequence=VSP_005463, VSP_005464;

CC Name=BMP1-5;

CC IsoId=P13497-4; Sequence=VSP_005465, VSP_005466;

CC Name=BMP1-6;

CC IsoId=P13497-5; Sequence=VSP_005467, VSP_005468;

CC Name=BMP1-7;

CC IsoId=P13497-6; Sequence=VSP_005469, VSP_005470;

CC -1- TISSUE SPECIFICITY: Ubiquitous.

CC -1- SIMILARITY: Belongs to peptidase family M12A.

CC -1- SIMILARITY: Contains 2 EGF-like domains.

CC -1- SIMILARITY: Contains 5 CUB domains.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ch/announce/> or send an email to license@sb.ebi.ch).

CC -----

CC EMBL; U50330; AAA93462.1; -

CC EMBL; M22488; AAA51833.1; -

CC EMBL; Y08723; CAA69973.1; -

CC EMBL; Y08724; CAA69974.1; -

CC EMBL; Y08725; CAA69975.1; -

CC EMBL; L35278; AAC41703.1; -

CC EMBL; L35279; AAC41710.1; -

CC PIR; A37278; B58788.

CC HSSP; P00736; IAPQ.

CC MEROPS; M12.005; -

CC Genew; HGNC:1067; BMP1.

CC MIM; 112264; -

CC GO; GO:0005576; C:extracellular; NAS.

CC GO; GO:0008237; F:metallopeptidase activity; NAS.

CC GO; GO:0001502; P:cartilage condensation; TAS.

CC GO; GO:0007275; P:development; TAS.

CC InterPro; IPR000152; Asx_hydroxyl_S.

CC InterPro; IPR001881; EGF_Ca.

CC InterPro; IPR000859; CUB.

CC InterPro; IPR006209; EGF_Like.

CC InterPro; IPR006025; Pept_M_Zn_BS.

CC InterPro; IPR006026; Peptidase_M.

CC InterPro; IPR001506; Peptidase_M12A.

CC Pfam; PF00431; CUB; 5.

CC Pfam; PF00008; EGF; 2.

CC PRINTS; PRO0460; ASTACIN.

CC SMART; SM00042; CUB; 5.

CC SMART; SM00179; EGF_CA; 2.

CC SMART; SM00235; ZnMC; 1.

CC PROSITE; PS00010; ASX_HYDROXYL; 2.

CC PROSITE; PS00180; CUB; 5.

CC PROSITE; PS00022; EGF_1; FALSE_NEG.

CC PROSITE; PS01186; EGF_2; 2.

CC PROSITE; PS05026; EGF_3; 2.

CC PROSITE; PS01187; EGF_CA; 2.

CC PROSITE; PS00142; ZINC_PROTEASE; 1.

CC Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;

CC Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;

CC Glycoprotein; Zymogen; Alternative splicing.

CC SIGNAL

CC PROPEP 1 22

CC PROPEP 23 120

CC CHAIN 121 986

CC CHAIN 121 321

CC DOMAIN 322 434

CC DOMAIN 435 546

CC DOMAIN 547 588

CC DOMAIN 591 703

CC DOMAIN 704 743

CC DOMAIN 747 859

CC CUB 1.

CC CUB 2.

CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

CC CUB 3.

CC EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

CC CUB 4.

```

FT DOMAIN 860 976 CUB 5.
FT METAL 213 213 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 214 214 BY SIMILARITY.
FT METAL 217 217 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 223 223 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 183 186 BY SIMILARITY.
FT DISULFID 322 348 BY SIMILARITY.
FT DISULFID 375 397 BY SIMILARITY.
FT DISULFID 435 461 BY SIMILARITY.
FT DISULFID 488 510 BY SIMILARITY.
FT DISULFID 551 563 BY SIMILARITY.
FT DISULFID 559 572 BY SIMILARITY.
FT DISULFID 574 587 BY SIMILARITY.
FT DISULFID 591 617 BY SIMILARITY.
FT DISULFID 644 666 BY SIMILARITY.
FT DISULFID 707 718 BY SIMILARITY.
FT DISULFID 714 727 BY SIMILARITY.
FT DISULFID 729 742 BY SIMILARITY.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 599 599 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 703 730 DKDCSKDNGCCQDDCVNTFGSYECQCR -> EKRALOPP
RGRPHQKFRVQKRNRPQ (in isoform BMP1-1).
FT VARSPLIC 731 986 /FtId=VSP 005461.
Missing (in isoform BMP1-1).
FT VARSPLIC 245 302 /FtId=VSP 005462.
Missing (in isoform BMP1-1).
FT VARSPLIC 303 986 /FtId=VSP 005464.
Missing (in isoform BMP1-4).
FT VARSPLIC 589 622 /FtId=VSP 005465.
Missing (in isoform BMP1-5).
FT VARSPLIC 623 986 /FtId=VSP 005466.
Missing (in isoform BMP1-5).
FT VARSPLIC 703 717 /FtId=VSP 005467.
Missing (in isoform BMP1-6).
FT VARSPLIC 718 986 /FtId=VSP 005468.
Missing (in isoform BMP1-6).
FT VARSPLIC 703 823 /FtId=VSP 005469.
Missing (in isoform BMP1-7).
FT VARSPLIC 824 986 /FtId=VSP 005470.
Missing (in isoform BMP1-7).
FT CONFLICT 748 748 D -> N (IN REF. 4).
FT CONFLICT 934 934 R -> S (IN REF. 4).
SQ SEQUENCE 986 AA; 111248 MW; F89201913K3CBEA CRC64;

```

Query Match 9.8%; Score 181; DB 1; Length 986;
 Best Local Similarity 42.6%; Pred. No. 7.4e-07;
 Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

```

QY 55 NSGSHPKPHTPTPRMNVLVAVDENRILQTDDEFGLEDPEDDICKDFVEER 113
DB 599 NSGSHPKPHTPTPRMNVLVAVDENRILQTDDEFGLEDPEDDICKDFVEER 654
QY 114 -PSDGSVLGRWCGSGTVPGKOTSKGNHRIKRVFSDVEPSEPCCHY 160
DB 655 LTRDSKLHGKFGCS-EKPEVITTSQYNNMRYVEFSKSDNTV-SKSGFKAHF 700

```

```

RESULT 4
ID BMP1_MOUSE STANDARD; PRT; 991 AA.
AC P98053;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 1 precursor (BC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mrlid).
GN BMP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=94229342; PubMed=8174772;
RA Fukagawa M., Nobori S., Hogan B.L.M., Jones C.M.;
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT which is related to the Drosophila dorsventral gene tollid and
RT encodes a putative astracin metalloendopeptidase.";
RL Dev. Biol. 163:175-183(1994).
CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC and III. Induces cartilage and bone formation.
CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala-I-asp in type I and II procollagens and at Arg-I-asp in type
CC III.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-
CC endopeptidase enhancer protein.
CC -1- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC and floor plate region of the neural tube. Less in developing
CC membranous and endochondral bone, submucosa of intestine, dermis
CC of skin and the mesenchyme of spleen and lung.
CC -1- SIMILARITY: Belongs to peptidase family M12a.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 5 CUB domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L24785; AAA37306.1; -.
DR PIR; I49540; I49540.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.005; -.
DR MCD; MGI:88176; BMP1.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12a.
DR Pfam; PF01400; Astracin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.

```

KM Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
 KM Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
 KM Glycoprotein; Zymogen.
 FT SIGNAL 1 25
 FT PROPEP 26 125
 FT CHAIN 126 991
 FT DOMAIN 126 326
 FT DOMAIN 327 439
 FT DOMAIN 440 551
 FT DOMAIN 552 593
 FT DOMAIN 596 707
 FT DOMAIN 708 748
 FT DOMAIN 752 864
 FT DOMAIN 865 981
 FT METAL 218 218
 FT ACT_SITE 219 219
 FT METAL 222 222
 FT METAL 228 228
 FT DISULFID 188 191
 FT DISULFID 327 353
 FT DISULFID 380 402
 FT DISULFID 440 466
 FT DISULFID 493 515
 FT DISULFID 556 568
 FT DISULFID 564 577
 FT DISULFID 579 592
 FT DISULFID 596 622
 FT DISULFID 649 671
 FT DISULFID 712 723
 FT DISULFID 719 732
 FT DISULFID 734 747
 FT CARBOHYD 96 96
 FT CARBOHYD 147 147
 FT CARBOHYD 337 337
 FT CARBOHYD 368 368
 FT CARBOHYD 604 604
 SO SEQUENCE 991 AA; 111607 MW; 68A1847783A0B9E CRC64;

Query Match 9.8%; Score 181; DB 1; Length 991;
 Best Local Similarity 42.6%; Pred. No. 7.5e-07;
 Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

QY 55 NGSIHSPKPTFPRNMYLVAVDENVRIQLTFDRFGLEDEDDICKYDFVEVE- 113
 DB 604 NGSTTSPEWPKETPRNKNCIMQLVAFTQ-YRISLQFD--PPEBGNVCKDYFEVAVSG 659

QY 114 -PDSGSYLGRWCGSGTVPGKOTSKGNHIRIRFVSDPEPSEPGFCIH 160
 DB 660 LTADSKLHGKFCGS-EKPEVITSGNNMRVFEKSDNTV-SKKGFRAHF 705

RESULT 5
 NRPI_HUMAN STANDARD; PRT; 923 AA.
 AC 014786; 060461;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
 GN NRPI OR NRP OR VEGF165R.
 OS Homo sapiens (Human).
 CC Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=97433084; PubMed=9288753;
 RA He Z., Tessier-Lavigne M.,
 RT "Neuropilin is a receptor for the axonal chemorepellent semaphorin
 RL III.";
 RL Cell 90:739-751(1997).
 [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.
 RC TISSUE=Brain;
 RX MEDLINE=96186099; PubMed=9529250;
 RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
 RT "Neuropilin-1 is expressed by endothelial and tumor cells as an
 RT isoform-specific receptor for vascular endothelial growth factor.";
 RL Cell 92:735-745(1998).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.
 RC TISSUE=Prostatic adenocarcinoma;
 RX MEDLINE=20183929; PubMed=10688880;
 RA Gagnon M.L., Bieleman D.R., Gechtman Z., Miao H.-Q., Takashima S.,
 RA Soker S., Klagsbrun M.;
 RT "Identification of a natural soluble neuropilin-1 that binds vascular
 RT endothelial growth factor: In vivo expression and antitumor
 RT activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).
 [4]
 RP CHARACTERIZATION.
 RX MEDLINE=20309748; PubMed=10748121;
 RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
 RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
 RT form of vascular endothelial growth factor (VEGF) and of placenta
 RT growth factor-2, but only neuropilin-2 functions as a receptor for
 RT the 145-amino acid form of VEGF.";
 RL J. Biol. Chem. 275:18040-18045(2000).
 CC -1- FUNCTION: The membrane-bound isoform 1 is a receptor involved in
 CC the development of the cardiovascular system, in angiogenesis, in
 CC the formation of certain neuronal circuits and in organogenesis
 CC outside the nervous system. It mediates the chemorepellant
 CC activity of semaphorins. It binds to semaphorin 3A, The PLGF-2
 CC isoform of bFGF, The VEGF-165 isoform of VEGF and VEGF-B.
 CC Coexpression with KDR results in increased VEGF-165 binding to KDR
 CC as well as increased chemotaxis. It may regulate VEGF-induced
 CC angiogenesis.
 CC -1- FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to
 CC inhibit its binding to cells. It may also induce apoptosis by
 CC sequestering VEGF-165. May bind as well various members of the
 CC semaphorin family. Its expression has an aversive effect on blood
 CC vessel number and integrity.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
 CC secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Membrane-bound;
 CC IsoId=014786-1; Sequence=Displayed;
 CC Name=2; Synonyms=Soluble, SNRP1;
 CC IsoId=014786-2; Sequence=VSP_004339, VSP_004340;
 CC -1- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not
 CC seem to overlap. Isoform 1 is expressed by the blood vessels of
 CC different tissues. In the developing embryo it is found
 CC predominantly in the nervous system. In adult tissues, it is
 CC highly expressed in heart and placenta; moderately in lung, liver,
 CC skeletal muscle, kidney and pancreas; and low in adult brain.
 CC Isoform 2 is found in liver hepatocytes, kidney distal and
 CC proximal tubules.
 CC -1- SIMILARITY: Belongs to the neuropilin family.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: Contains 1 MM domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL; AF018956; AAC51759.1; -;
 CC DR EMBL; AF016050; AAC12921.1; -;
 CC DR EMBL; AF145712; AAF44344.1; -;
 CC DR PDB; 1KEX; 28-JAN-03.

DR	Genew;	HGNc:8004;	NRP1.	
DR	MIM:	602069;	-	
DR	GO:	GO:0005021;	F-vascular endothelial growth factor receptor. . .;	TAS.
DR	GO:	GO:0007411;	Paxon guidance; TAS.	
DR	GO:	GO:0007267;	P-cell-cell signaling; TAS.	
DR	GO:	GO:0007397;	Phitogenesis and organogenesis; TAS.	
DR	GO:	GO:0008288;	P-ositve regulation of cell proliferation; TAS.	
DR	GO:	GO:0007165;	P-signal transduction; TAS.	
DR	InterPro:	IPR000859;	CUB.	
DR	InterPro:	IPR000421;	FA58_C.	
DR	InterPro:	IPR008979;	Gal_Bind_like.	
DR	InterPro:	IPR000998;	MAM_domain.	
DR	Pfam:	PF00431;	CUB; 2.	
DR	Pfam:	PF00754;	FS_F8_type_C; 2.	
DR	PRINTS:	PR00020;	MAMDOMAIN.	
DR	SMART:	SM00042;	CUB; 2.	
DR	SMART:	SM00231;	FA58C; 2.	
DR	SMART:	SM00137;	MAM; 1.	
DR	PROSITE:	PS01180;	CUB; 2.	
DR	PROSITE:	PS01285;	FA58C_1; 2.	
DR	PROSITE:	PS01286;	FA58C_2; 2.	
DR	PROSITE:	PS50022;	FA58C_3; 2.	
DR	PROSITE:	PS00740;	MAM_1; 1.	
DR	PROSITE:	PS50060;	MAM_2; 1.	
KW	Angiogenesis;	Transmembrane;	Glycoprotein; Neurone; Signal; Repeat;	
KW	Receptor;	Alternative splicing;	3D-structure.	
FT	SIGNAL	1	21	
FT	CHAIN	22	923	
FT	DOMAIN	22	856	NEUROPILIN-1.
FT	TRANSMEM	857	879	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	880	923	POTENTIAL.
FT	DOMAIN	27	141	CYTOSOLASMIC (POTENTIAL).
FT	DOMAIN	147	265	CUB 1.
FT	DOMAIN	275	424	CUB 2.
FT	DOMAIN	431	583	FS/8 TYPE C 1.
FT	DOMAIN	645	811	FS/8 TYPE C 2.
FT	DISULFID	27	54	MM.
FT	DISULFID	82	104	PROBABLE.
FT	DISULFID	147	173	PROBABLE.
FT	DISULFID	206	228	PROBABLE.
FT	DISULFID	275	424	PROBABLE.
FT	DISULFID	431	583	BY SIMILARITY.
FT	DISULFID	150	150	BY SIMILARITY.
FT	CARBOHYD	251	261	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	522	522	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	842	842	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VANSPPLIC	642	644	EFP -> GIK (in isoform 2).
FT	VANSPPLIC	645	923	/FTid-VSP 004339.
FT	VANSPPLIC	645	923	Missing (in isoform 2).
FT	CONFLICT	26	26	K -> E (IN REF. 1).
FT	CONFLICT	749	749	D -> H (IN REF. 2).
FT	CONFLICT	855	855	E -> D (IN REF. 2).
QO	SEQUENCE	923 AA;	103120 MW;	ADBADQ4A949B5D57 CRC64;

```

Query Match      9.5%; Score 176; DB 1; Length 923;
Best Local Similarity 32.6%; Pred. No. 1.8e-06;
Matches 57; Conservative 24; Mismatches 68; Indels 26; Gaps 9.

QY VTISGNGSIHSPKPEPTYPRMNVLVWRIVAVDENVRIOLTTPFERGLEDEPEDICKYDFV 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  31 IKIESPGVLTSPGHSHYHPSEKCMWLIQADPYRIMINFPNPHDLERD---CKYIV 87
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 110 EV--EESPDSVLGRGSGTVPGKQTSKGNHRIIRFVSDXEYFSPSGCIHYSITM--P 165
   - - - - - : : : : : : : : : : : : : : : : : : : : : :
Db  88 EVFDGEMNGHGRGKFCCK-IAPPVWSSGPIFLFKFSD-YETHGAGSIYVEIIFKRG 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 166 QVTE--TTPSPVLP-----PSSLIDLNNATVAFSTLEELIRY---LEPD 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  146 ECSQVYTTTPSGVTKRGPFPEKYPNSLSECTY---VFAPKMSIILIEFSSFLDEP 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

ID	TID	BRARE	STANDARD;	PRT;	1022	AA.
AC	057460;					
DT	16-OCT-2001	(Rel. 40, Created)				
DT	16-OCT-2001	(Rel. 40, Last sequence update)				
DT	16-OCT-2001	(Rel. 40, Last annotation update)				
DE	Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)					
DE	(Mn1 fin protein)					
GN	TOLLOID OR TLD OR MFN.					
OS	Brachydano rerio (Zebrafish) (Danio rerio).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;					
OC	Cyprinidae; Danio.					
OX	NCBI_TaxID=7955;					
RN	[1]					
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.					
RC	TISSUE=Gastrula;					
RX	MEDLINE=98057457; PubMed=9395394;					
RA	Blader P., Rastegar S., Fischer N., Straehle U.;					
RT	"Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid.";					
RL	Science 278:1937-1940(1997).					
RN	[2]					
RP	FUNCTION, AND TISSUE SPECIFICITY.					
RX	MEDLINE=99307076; PubMed=10375503;					
RA	Connors S.A., Trout J., Ekker M.C.;					
RT	"The role of tolloid/mn1 fin in dorsoventral pattern formation of the zebrafish embryo.";					
RL	Development 126:3119-3130(1999).					
CC	-1- FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic protein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP from inactive complexes.					
CC	-1- TISSUE SPECIFICITY: During gastrulation, accumulates around the closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-somite stage, expressed in the developing tailbud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoietic system.					
CC	-1- SIMILARITY: Belongs to peptidase family M12A.					
CC	-1- SIMILARITY: Contains 2 EGF-like domains.					
CC	-1- SIMILARITY: Contains 5 CUB domains.					
CC	-----					
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL;	AF027596;	AAC60304.1;	--		
DR	HSSP;	P35555;	1EMN.			
DR	MEROPS;	M12.016;	--			
DR	ZFIN;	ZDB-GENE-990415-265;	tolloid.			
DR	InterPro;	IPR000152;	Asx_hydroxy1_S.			
DR	InterPro;	IPR000859;	CUB.			
DR	InterPro;	IPR001881;	EGF_Ca.			
DR	InterPro;	IPR006209;	EGF_Like.			
DR	InterPro;	IPR006025;	Pept_M_Zn_BS.			
DR	InterPro;	IPR006026;	Peptidase_M.			
DR	InterPro;	IPR001506;	Peptidase_M12A.			
DR	Pfam;	PF01400;	Asiadin_1.			
DR	Pfam;	PF00431;	CUB_5.			
DR	Pfam;	PF00008;	EGF_2.			
DR	PRINTS;	PR00480;	ASTACIN.			
DR	SMART;	SM00042;	CUB_5.			
DR	SMART;	SM00179;	EGF_CA_2.			
DR	SMART;	SM00235;	ZDMC_1.			
DR	PROSITE;	PS00010;	ASX_HYDROXYL_2.			
DR	PROSITE;	PS01180;	CUB_5.			
DR	PROSITE;	PS00022;	EGF_1;	FALSE	NEG	

FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 922 AA; 103082 MW; CCF6F2AD098B0F2E CRC64;
 Query Match 9.3%; Score 172; DB 1; Length 922;
 Best Local Similarity 31.5%; Pred. No. 3.7e-06;
 Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;
 QY 2 LLLGLLLTSLALAGQRTGTRAESNLSSKQLQSDKEQNGVQDPHRRHVTTISGNSIHSP 61
 DB 7 LLCATLALALALAG-----AFRSKCGG-----TIKENPGYLTSP 42
 QY 62 KPEHTTFRNMVWLRVAVDENVRIQLTDERGLEDDEDDICKYDFVEV--EPPSDGSV 119
 DB 43 GYHSYHPSKCEWLIQAPFPYQRIINFPNPHLEDRD---CKDYVEVIDGENEGRL 99
 QY 120 LGRWCGSGTVPGKQTSKGNHRIREFVSDYFPEPFCIHYSIIM--PQTER--TSPS 174
 DB 100 WGFKCGK-IAPSPVSSGPFPIKFVSD-YETHGAGFSIRYELFKRGPECSQNYTAPT 155
 RESULT 8
 NRPI_MOUSE STANDARD; PRT; 923 AA.
 AC P97333;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropilin-1 precursor (A5 protein).
 GN NRPI OR NRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Embryonic brain;
 RA MEDLINE=96353149; PubMed=8748368;
 RX Kawakami A., Kitsuikawa T., Takagi S., Fujisawa H.;
 RT "Developmentally regulated expression of a cell surface protein,
 RT neuropilin, in the mouse nervous system.";
 RL J. Neurobiol. 29:1-17(1996).
 CC - FUNCTION: Receptor involved in the development of the
 CC cardiovascular system, in angiogenesis, in the formation of
 CC certain neuronal circuits and in organogenesis outside the nervous
 CC system. It mediates the chemorepulsive activity of semaphorins. It
 CC binds to semaphorin 3A, the PlGF-2 isoform of bFGF, the VEGF-165
 CC isoform of VEGF and VEGF-B. Coexpression with KDR results in
 CC increased VEGF-165 binding to KDR as well as increased chemotaxis.
 CC It may regulate VEGF-induced angiogenesis (By similarity).
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - TISSUE SPECIFICITY: Nervous system.
 CC - SIMILARITY: Belongs to the neuropilin family.
 CC - SIMILARITY: Contains 2 CUB domains.
 CC - SIMILARITY: Contains 1 MAM domain.
 CC - SIMILARITY: Contains 1 MAM domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D50086; BAA08789.1; -.
 CC HSP: P12259; LCZT.
 CC MGD: MG1:106206; NRP.
 CC GO: GO:0017154; F:semaphorin receptor activity; IGI.
 CC InterPro: IPR000859; CUB.
 CC InterPro: IPR000421; FAS5 C.
 CC InterPro: IPR008979; GalBind like.
 CC InterPro: IPR000996; MAM_domain.

DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_P8_Type_C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FAS5C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FAS5C_1; 2.
 DR PROSITE; PS01286; FAS5C_2; 2.
 DR PROSITE; PS00022; FAS5C_3; 2.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR Angiogenesis; Transmembrane; Glycoprotein; Neurope; Signal; Repeat;
 KW Receptor.
 FT SIGNAL 1 21
 FT CHAIN 22 923
 FT DOMAIN 22 856
 FT TRANSMEM 857 879
 FT DOMAIN 880 923
 FT DOMAIN 27 141
 FT DOMAIN 147 265
 FT DOMAIN 275 424
 FT DOMAIN 431 583
 FT DOMAIN 645 811
 FT DISULFID 27 54
 FT DISULFID 82 104
 FT DISULFID 147 173
 FT DISULFID 206 228
 FT DISULFID 275 424
 FT CARBOHYD 431 583
 FT CARBOHYD 150 150
 FT CARBOHYD 261 261
 FT CARBOHYD 300 300
 FT CARBOHYD 522 522
 FT CARBOHYD 842 842
 SQ SEQUENCE 923 AA; 103020 MW; 0644B8A17096808 CRC64;
 Query Match 9.1%; Score 169; DB 1; Length 923;
 Best Local Similarity 31.5%; Pred. No. 6.5e-06;
 Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;
 QY 2 LLLGLLLTSLALAGQRTGTRAESNLSSKQLQSDKEQNGVQDPHRRHVTTISGNSIHSP 61
 DB 7 LLCATLALALALAG-----AFRSKCGG-----TIKENPGYLTSP 42
 QY 62 KPEHTTFRNMVWLRVAVDENVRIQLTDERGLEDDEDDICKYDFVEV--EPPSDGSV 119
 DB 43 GYHSYHPSKCEWLIQAPFPYQRIINFPNPHLEDRD---CKDYVEVIDGENEGRL 99
 QY 120 LGRWCGSGTVPGKQTSKGNHRIREFVSDYFPEPFCIHYSIIM--PQTER--TSPS 174
 DB 100 WGFKCGK-IAPSPVSSGPFPIKFVSD-YETHGAGFSIRYELFKRGPECSQNYTAPT 155
 RESULT 9
 NRPI_CHICK STANDARD; PRT; 914 AA.
 ID NRPI_CHICK
 AC P97975;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuropilin-1 precursor (A5 protein).
 GN NRPI OR NRP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Embryonic brain;
 RX MEDLINE=95324761; PubMed=7601310;

RA Takagi S., Kasuya Y., Shimizu M., Matsura T., Tsuboi M., Kawakami A.,
 RA Fujisawa H.;
 RT "Expression of a cell adhesion molecule, neuropilin, in the
 RT developing chick nervous system.";
 RL Dev. Biol. 170:207-222(1995).
 CC -1- FUNCTION: Receptor involved in the development of the
 CC cardiovascular system, in angiogenesis, in the formation of
 CC certain neuronal circuits and in organogenesis outside the nervous
 CC system. It mediates the chemorepulsive activity of semaphorins (By
 CC similarity). Seems to have calcium-independent cell adhesion
 CC properties.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Developing nervous system; optic tectum
 CC (layers D and E of SGFS), amacrine cells of retina, neurites of
 CC dorsal root ganglia. Also expressed in nonneuronal cells, e.g.
 CC blood vessels in the entire embryo.
 CC -1- SIMILARITY: Belongs to the neuropilin family.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: Contains 1 MAM domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D45416; BAA08256.1; -;
 CC DR HSSP: P12259; 1CZT.
 CC DR InterPro: IPR000859; CUB.
 CC DR InterPro: IPR000421; FAS8_C.
 CC DR InterPro: IPR008979; Gal_Bind_Like.
 CC DR InterPro: IPR000998; MAM_domain.
 CC DR Pfam: PF00431; CUB; 2.
 CC DR Pfam: PF00754; F5_F8_Type_C; 2.
 CC DR Pfam: PF00629; MAM; 1.
 CC DR PRINTS: PRO0020; MAMDOMAIN.
 CC DR SMART: SM00042; CUB; 2.
 CC DR SMART: SM00231; FAS8C; 2.
 CC DR SMART: SM00137; MAM; 1.
 CC DR PROSITE: PS01180; CUB; 2.
 CC DR PROSITE: PS01285; FAS8C_1; 2.
 CC DR PROSITE: PS01286; FAS8C_2; 2.
 CC DR PROSITE: PS50022; FAS8C_3; 2.
 CC DR PROSITE: PS00740; MAM_1; 1.
 CC DR PROSITE: PS50060; MAM_2; 1.
 CC DR Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
 CC KM Receptor; Cell adhesion.
 CC KW SIGNAL 1
 CC FT CHAIN 18
 CC FT CHAIN 19 914
 CC FT DOMAIN 20 847
 CC FT TRANSMEM 848 870
 CC FT DOMAIN 871 914
 CC FT DOMAIN 25 139
 CC FT DOMAIN 145 263
 CC FT DOMAIN 273 422
 CC FT DOMAIN 429 581
 CC FT DOMAIN 636 801
 CC FT DISULFID 25 52
 CC FT DISULFID 80 102
 CC FT DISULFID 145 171
 CC FT DISULFID 204 226
 CC FT DISULFID 273 422
 CC FT DISULFID 429 581
 CC FT DISULFID 581 914
 CC FT DISULFID 914 AA; 102480 MW; DD2BE6DF0CB868C CRG64;
 CC SEQUENCE
 CC Query Match 9.0%; Score 167; DB 1; Length 914;
 CC Best Local Similarity 28.8%; Pred. No. 9.4e-06;
 CC Matches 51; Conservative 31; Mismatch 65; Indels 30; Gaps 9;
 CC 50 VTISGNSHSPKPHPTPRNMVAVVAVDEVRVQLFDEKFGAEDDEDDICKYDFV 109

DB 29 IKILSPYLTPSPGPOSHYSQCEMLIQAPPEYQRIIMINPNFDEDD---CKYDYV 85
 QY 110 EV--EESPDSVUGRMCGSGTVPCKQTSKNHRIKRVSEYPPSEGFCHISITN--P 165
 DB 86 EVIDGDNAEERLRWKGKCGK-IAPPPLVSSGPYLFIKFKV-YETHGAGFSIRYEVFRGP 143
 QY 166 QYVE--TTSVSLP-----PSSSLD-----LNNVTAFTLEELIRYLEPD 206
 DB 144 ECKNFITSSGMIKSPGPKPKYFNSLCTYIIRAPKMSLILEPSE-----LEPD 195
 RESULT 10
 ID SPAN_STRPU STANDARD; PRT; 616 AA.
 AC P98068;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DE SPAN protein precursor (EC 3.4.24.-).
 GN SPAN.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RX MEDLINE=92315921; PubMed=1618141;
 RA Reynolds S.D., Angerer L.M., Pails J., Nasir A., Angerer R.C.;
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of
 RT sea urchin embryos, include one encoding a protein related to tollid
 RT and BMP-1.";
 RL Development 114:769-786(1992).
 CC -1- TISSUE SPECIFICITY: Asymmetrically along the animal-vegetal axis
 CC of the blastula.
 CC -1- DEVELOPMENTAL STAGE: Very early blastula (between 16-cell stage
 CC and hatching).
 CC -1- SIMILARITY: Belongs to peptidase family M12A.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M84144; AAA30072.1; -;
 CC DR HSSP: P28825; 1IAF.
 CC DR MEROPS: M12_013; -;
 CC DR InterPro: IPR000859; CUB.
 CC DR InterPro: IPR006209; EGF_Like.
 CC DR InterPro: IPR006210; IEGF_Like.
 CC DR InterPro: IPR006025; Pept_M_Zn_BS.
 CC DR InterPro: IPR006026; Peptidase_M.
 CC DR InterPro: IPR001506; Peptidase_M12A.
 CC DR Pfam: PF00431; Astacin; 1.
 CC DR Pfam: PF00431; CUB; 2.
 CC DR PRINTS: PRO0480; ASTACIN.
 CC DR SMART: SM00042; CUB; 2.
 CC DR SMART: SM00181; EGF; 1.
 CC DR SMART: SM00235; ZNMG; 1.
 CC DR PROSITE: PS01180; CUB; 2.
 CC DR PROSITE: PS00022; EGF_1; 1.
 CC DR PROSITE: PS01186; EGF_2; 1.
 CC DR PROSITE: PS50026; EGF_3; 1.
 CC DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC KM Developmental protein; Repeat; Hydroxylase; Protease; Zinc; Embryo;
 CC Metalloprotease; EGF-like domain; Signal.
 CC FT SIGNAL 1
 CC FT SIGNAL 16
 CC POTENTIAL.

```

FT PROPEP 17 93 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 94 616 SPAN PROTEIN.
FT DOMAIN 93 295 ARG/LYS-RICH (BASIC).
FT DOMAIN 94 295 METALLOPROTEASE.
FT DOMAIN 295 329 EGF-LIKE.
FT DOMAIN 340 450 CUB 1.
FT DOMAIN 451 502 THR-RICH.
FT DOMAIN 503 614 CUB 2.
FT METAL 190 190 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 191 191 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 194 194 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 200 200 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 299 315 BY SIMILARITY.
FT DISULFID 305 317 BY SIMILARITY.
FT DISULFID 319 328 BY SIMILARITY.
SQ SEQUENCE 616 AA; 67902 MW; 397CD923F9B98 CRC64;

Query Match 8.88; Score 163.5; DB 1; Length 616;
Best Local Similarity 28.04; Pred. No. 1.1e-05;
Matches 63; Conservative 30; Mismatches 85; Indels 47; Gaps 11;

QY 9 LTSALAGORTG-TRASNLSKQLSDDX-----ONGVODRHRHV--TISGN- 55
DB 269 LNSRL-GQRTALSAADIELNRIYECDDVEDCSNADECLANGYHDDCCVCPSSYSGLD 327
QY 56 -----GSIHSPKPPHTYPRNVLVWRLVAVDENVRIOQTDERF 94
DB 328 CODGFTVRPADCSYRFTMTGETITSPNSNEDMTACVYELEG-PYGSTIELTF---L 383
QY 95 GLEDEPDIDCKYFVEVEEEDSGVIGRCWCGSGTGVKQTSKNHRIKRVSDVEYPPS-- 152
DB 384 DMEIEETELCRVAEVRKDDINSIEKFCGN-TLPPVOQISSNOMWVSFTSD---PSIT 439
QY 153 EPGFCIHSYIIMPQVT--ETTSPSVPPSSLSLDLNNATVAST 195
DB 440 RRGFKATYVILIIQTTVFSTITLQTTPTSTTTLQTTNPTSTTLQTT 484

RESULT 11
PCOL HUMAN STANDARD; PRT; 449 AA.
AC 015113; 014550;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-
DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler B., Biniamnov L., Brusel M., Eddy R.L.,
RA Jani-Sait S., Shows T.B., Greenspan D.S.,
RT "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RL J. Biol. Chem. 269:26280-26285 (1994).
RN [2]
RP REVISIONS TO 56; 154 AND 373.
RA Kessler B.;
RL unpublished observations (FSB-2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX Hishara I., Syoutuda K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.,
RT "smooth muscle cell derived procollagen C-protease enhancer protein.";

```

```

RL Cell Struct. Funct. 21:662-662(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Glocker G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.,
RT "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUB1 loci
RT reveals 17 genes.";
RL Genome Res. 8:1060-1073(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99134301; PubMed=9933570;
RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.,
RT "Structural organization and expression patterns of the human and
RT mouse genes for the type I procollagen COOH-terminal proteinase
RT enhancer protein.";
RL Genomics 55:229-234(1999).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Caavaant T.L., Scheetz T.E.,
RA Brownstein M.U., Ussid T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
RX MEDLINE=20092917; PubMed=10625689;
RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
RA Banda M.J.,
RT "Post-translational proteolytic processing of procollagen C-terminal
RT proteinase enhancer releases a metalloproteinase inhibitor.";
RL J. Biol. Chem. 275:1384-1390(2000).
RN [8]
RP FUNCTION: Binds to the COOH-terminal propeptide of type I
RN procollagen and enhances procollagen C-proteinase activity.
CC - FUNCTION: C-terminal processed part of PCPE (Ct-PCPE) may have an
CC metalloproteinase inhibitory activity.
CC - SUBCELLULAR LOCATION: Secreted.
CC - PTM: C-terminally processed at multiple positions.
CC - SIMILARITY: Contains 2 CUB domains.
CC - SIMILARITY: Contains 1 NTR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
DR EMBL; I33799; AAA61949.1; ALT SEQ.
DR EMBL; AB008549; BAA23281.1; -
DR EMBL; AF053356; AAC78800.1; -
DR EMBL; AF083655; AAD16041.1; -
DR EMBL; BC000574; AAH00574.1; -

```

```
CC lining in the ribs.
CC -1- SIMILARITY: Belongs to the neotropilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domain.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF016297; AAC53338.1; -.
CC HSSP; P12259; 1CZT.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000421; FA58_C.
CC InterPro; IPR008979; Gal_Bind_1like.
CC InterPro; IPR000998; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FA58C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FA58C_2; 2.
CC PROSITE; PS01286; FA58C_2; 2.
CC PROSITE; PSS0022; FA58C_3; 2.
CC PROSITE; PSS0060; MAM_2; 1.
CC Trasnmembrane; Glycoprotein; Neutrone; Signal; Repeat; Receptor.
KV SIGNAL 1 22
FT CHAIN 23 925 NEUROFILIN-2.
FT DOMAIN 23 858 EXTRACELLULAR (POTENTIAL).
FT TRANSERM 859 883 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 884 925 CUB 1.
FT DOMAIN 28 142 CUB 2.
FT DOMAIN 149 267 F5/8 TYPE C 1.
FT DOMAIN 277 427 F5/8 TYPE C 2.
FT DOMAIN 434 592 MAM.
FT DOMAIN 642 802 BY SIMILARITY.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 925 AA; 103896 MW; 3BFE2903F644851C CRC64;

Query March 8.4%; Score 155.5; DB 1; Length 925;
Best local Similarity 33.3%; Pred. No. 8.3e-05;
Matches 41; Conservative 19; Mismatches 56; Indels 7; Gaps 4;

QY 42 QDPRIHERVTVISGNSIHSPEKPHRYPPRMVLVLRVAVDENVRIQLTFDERFGLEDPED 101
Db 24 ODPFCGGRLSKDAGYITSPGYPODYSHONCEWVVYAPEPNCKIVLFNPHFIERKD - 82
QY 102 DICKYDPVEVVERESDDGS--VLGMCGSGGVTPGKQTSGNGHNRIRPVSDERFPSEPGCIH 159
Db 83 --KKYFIEIRDDSESADLGRGCH-IAPPTISSGSVLYIKFTSD-YAEOGAQPSLR 138
QY 160 YSI 162
Db 139 YEI 141
```

RESULT 13
 NRP2 HUMAN STANDARD; PRT; 931 AA.
 AC 060462; 014820; 014821;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neupillin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
 GN NRP2 OR VEGF165R2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
 RX MEDLINE=97470888; PubMed=9333348;
 RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
 RT "Neupillin-2, a novel member of the neupillin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III.";
 RL Neuron 19:547-559(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A22).
 RC TISSUE=Breast;
 RX MEDLINE=98188099; PubMed=9529250;
 RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
 RT "Neupillin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";
 RL Cell 92:735-745(1998).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=20309748; PubMed=10748121;
 RA Guzman-Polcorak Z., Cohen T., Herzog Y., Neufeld G.;
 RT "Neupillin-2 and neupillin-1 are receptors for the 155-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neupillin-1 functions as a receptor for the 145-amino acid form of VEGF.";
 RL J. Biol. Chem. 275:18040-18045(2000).
 CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165 and VEGF-145 isoforms of VEGF, and the PlGF-2 isoform of PGF.
 CC -1- SUBUNIT: Neupillin-2 probably forms a heteromeric complex with neupillin-1 in order to be a functional semaphorin 3C receptor.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=A22;
 CC IsoId=O60462-1; Sequence=Displayed;
 CC Name=A0;
 CC IsoId=O60462-2; Sequence=VSP_004342;
 CC Name=A17;
 CC IsoId=O60462-3; Sequence=VSP_004341;
 CC -1- SIMILARITY: Belongs to the neupillin family.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: Contains 1 MAM domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF022859; AAC51788.1; -
 DR EMBL; AF022860; AAC51789.1; -
 DR EMBL; AF016098; AAC12922.1; -
 DR HSSP; P12259; IC2T.
 DR Genew; HGNC:8005; NRP2.
 DR MIM; 602070; -
 DR GO; GO:0005624; Cmembrane fraction; TAS.
 DR GO; GO:0004872; F;receptor activity; TAS.

DR GO; GO:0005021; F;vascular endothelial growth factor receptor. . .; TAS.
 DR GO; GO:007411; P;axon guidance; TAS.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000421; FAS5 C.
 DR InterPro; IPR008979; Gal_Bind_Like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FAS5C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FAS5C_1; 2.
 DR PROSITE; PS01286; FAS5C_2; 2.
 DR PROSITE; PS50022; FAS5C_3; 2.
 DR PROSITE; PS50060; MAM_2; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
 KW Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 1 931
 FT DOMAIN 21 931
 FT TRANSMEM 21 864
 FT TRANSMEM 865 889
 FT DOMAIN 890 931
 FT DOMAIN 28 142
 FT DOMAIN 149 267
 FT DOMAIN 277 427
 FT DOMAIN 434 592
 FT DOMAIN 642 802
 FT DOMAIN 671 674
 FT DISULFID 28 55
 FT DISULFID 133 105
 FT DISULFID 149 175
 FT DISULFID 208 230
 FT DISULFID 277 427
 FT DISULFID 434 592
 FT CARBOHYD 152 152
 FT CARBOHYD 157 157
 FT CARBOHYD 629 629
 FT CARBOHYD 839 839
 FT VARSPPLIC 809 813
 FT FT
 FT VARSPPLIC 809 830
 FT FT
 FT .CONFLICT 602 602
 FT SEQUENCE 931 AA; 104830 MM; 270CBAB6A0A797C CRC64;
 SQ
 Query Match 8.4%; Score 155.5; DB 1; Length 931;
 Best Local Similarity 32.1%; Pred. No. 8.4e-05;
 Matches 42; Conservative 20; Mismatches 62; Indels 7; Gaps 4;
 QY 34 SSKKQGVQDPDRHENVITSSGSIHSPKFTPTPRNVLVAVDENVRIQLTPDER 93
 DB 16 SHQVRGQDPDPGGRGLNSKQAGYITSPGYPDYSHONCEWIVAPENQKIVNPFNH 75
 QY 94 FGLPEPDDICXDEVEVEPEPSDGS--VLGRVSGGTVPKQOTSXGNHRIKRVSDSEYFP 151
 DB 76 FIEIKHD---CKYDIHIRDGSESADLLGKHCN-IAPPTISSGMLYIKFTSD-VAR 130
 QY 152 SEFGFCIHYSI 162
 DB 131 QGAGSLRYEI 141
 RESULT 14
 NRP2 MOUSE STANDARD; PRT; 931 AA.
 ID NRP2 MOUSE
 AC 035375; 035373; 035374; 035376; 035377; 035378;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neupillin-2 precursor (Vascular endothelial cell growth factor 165

GN receptor 2) .
 OS NR2.
 OS Mus musculus (Mouse) .
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5) .
 RC STRAIN=BA6/C;
 RX MEDLINE=97470888; PubMed=9331348;
 RA "Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.,
 RT "Neurophilin-2, a novel member of the neurophilin family, is a high
 RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
 RT III.";
 RL Neuron 15:547-559(1997) .
 CC -1 FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
 CC and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of PGF.
 CC -1 SUBUNIT: Neurophilin-2 probably forms a heteromeric complex with
 CC neurophilin-1 in order to be a functional semaphorin E receptor.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=A22;
 CC IsoId=O35375-1; Sequence=Displayed;
 CC Name=A0;
 CC IsoId=O35375-2; Sequence=VSP_004344;
 CC Name=A5;
 CC IsoId=O35375-3; Sequence=VSP_004345;
 CC Name=A17;
 CC IsoId=O35375-4; Sequence=VSP_004343;
 CC Name=B0;
 CC IsoId=O35375-5; Sequence=VSP_004346;
 CC Name=B5;
 CC IsoId=O35375-6; Sequence=VSP_004347;
 CC -1 TISSUE SPECIFICITY: Expressed in developing CNS, PNS and in some
 CC nonneural tissues including limb buds, developing bones, muscles,
 CC intestinal epithelium, kidney, lung and submandibular gland.
 CC -1 DEVELOPMENTAL STAGE: The expression pattern is very dynamic and is
 CC developmentally regulated.
 CC -1 SIMILARITY: Belongs to the neurophilin family.
 CC -1 SIMILARITY: Contains 2 CUB domains.
 CC -1 SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1 SIMILARITY: Contains 1 MAM domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/isb-sib.ch>).
 CC or send an email to license@isb-sib.ch .
 CC -----
 CC EMBL, AF022856; AAC53379.1; -
 DR EMBL, AF022854; AAC53377.1; -
 DR EMBL, AF022855; AAC53378.1; -
 DR EMBL, AF022857; AAC53380.1; -
 DR EMBL, AF022858; AAC53381.1; -
 DR EMBL, AF022861; AAC53382.1; -
 DR HSSP, P12259; 1CCT.
 DR WGD, MGI:1100492; NRP2.
 DR InterPro, IPR000859; CUB.
 DR InterPro, IPR000421; FAS5 C.
 DR InterPro, IPR008979; Gal Bind. like.
 DR InterPro, IPR000998; MAM_domain.
 DR Pfam, PF00431; CUB; 2.
 DR Pfam, PF00754; F5_F8_type_C; 2.
 DR Pfam, PF00629; MAM; 1.
 DR PRINTS, PR00020; MAMDOMAIN.
 DR SMART, SMO0042; CUB; 2.
 DR SMART, SMO0231; FAS5C; 2.
 DR SMART, SMO0137; MAM; 1.
 DR PROSITE, PS01180; CUB; 2.
 DR PROSITE, PS01285; FAS5C_1; 2.

DR	PROSITE; PS01286; FA58C_3; 2.
DR	PROSITE; PS50022; FA58C_3; 2.
DR	PROSITE; PS50060; MAM_2; 1.
KW	Ttransmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor; Alternative splicing.
FT	SIGNAL 1 20
FT	CHAIN 21 931
FT	DOMAIN 21 864
FT	TRANSMEM 865 889
FT	DOMAIN 890 931
FT	DOMAIN 28 142
FT	DOMAIN 149 267
FT	DOMAIN 277 427
FT	DOMAIN 434 592
FT	DOMAIN 642 802
FT	DOMAIN 838 845
FT	DISULFID 28 55
FT	DISULFID 139 105
FT	DISULFID 149 175
FT	DISULFID 208 230
FT	DISULFID 277 427
FT	DISULFID 434 592
FT	CARBOHYD 152 152
FT	CARBOHYD 157 157
FT	CARBOHYD 629 629
FT	CARBOHYD 839 839
FT	VARSPLIC 809 813
FT	VARSPLIC 809 830
FT	VARSPLIC 814 830
FT	VARSPLIC 810 931
FT	VARSPLIC 814 931
FT	VARSPPLIC 814 931
FT	CONFLICT 786 786
FT	SEQUENCE 931 AA; 104558 MW; 76F2443R411D2F63 CRC64;
QY	Query Match 3.4%; Score 155.5; DB 1; Length 931;
Db	Best Local Similarity 3.8%; Pred. No. 8.4e-05;
Matches	43; Conservative 18; Mismatches 63; Indels 7; Gaps 4;
QY	34 SDKEONGVQDDRHRHERVTISGSGSIHSEKFPHTYPRMNVLVWLVAVDENRIQLTPDER 93
Db	16 SGHEVRSQQDDPPCCGRPNSSKDAGYTTSFGYQDPDSHQNCMEIYYAPBPNOKITLNFNP 75
QY	94 FGLDEPDDICKYQFVEVEEESPDSS-VLGAWCSGGTVPGKQTSKGNIIRIRFVSDEYFP 151
Db	76 FEIEHGMD--EKYPDIFIRDGDSSADILGHKCN-IAPPTITSSGSVLVIKFTSD-YAR 130
QY	152 SEPGFCINYSI 162
Db	131 QGAGPSLRLEYI 141
RESULT 15	
VEGD RAT	
AC 035Z51:	STANDARD; PRT; 326 AA.
DT 28-FEB-2003 (Rel. 41, Created)	
DT 28-FEB-2003 (Rel. 41, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	

DE	Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DR	growth factor) (FIGF).
CN	FlgR OR VEGFD.
ON	Rattus norvegicus (Rat).
OS	Euxyryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCB1_TaxId=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sprague-Dawley;
RA	Yamada Y., Hirata Y., Nezu J., Shitane M.;
RL	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
CC	- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC	and endothelial cell growth, stimulating their proliferation and
CC	migration and also has effects on the permeability of blood
CC	vessels. May function in the formation of the venous and lymphatic
CC	vascular systems during embryogenesis, and also in the maintenance
CC	of differentiated lymphatic endothelium in adults. Binds and
CC	activates VEGFR-3 (Flt4) receptor (By similarity).
CC	- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC	- PTM: Undergoes a complex proteolytic maturation which generates a
CC	variety of processed secreted forms with increased activity toward
CC	VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC	linked by disulfide bonds before secretion. The fully processed
CC	VEGF-D is composed mostly of two VEGF homology domains (VHDS)
CC	bound by non-covalent interactions (By similarity).
CC	- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF014827; AAB6557.1; .-
DR	HSSP; P15692; IVPD.
DR	InterPro; IPR004153; CXCXC_repeat.
DR	InterPro; IPR000072; PD_growth_factor.
DR	Pfam; PF03128; CXCXC_1.
DR	Pfam; PF00341; PDGF; 1.
DR	Prodrom; PD001629; PD_growth_factor; 1.
DR	SMART; SMO014; PDGF_1.
DR	PROSITE; PS00249; PDGF_1; 1.
DR	PROSITE; PS50278; PDGF_2; 1.
KW	Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
RW	Cleavage on pair of basic residues; Multigene family.
FT	SIGNAL
FT	PROPEP
FT	CHAIN
FT	DOMAIN
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DIUPLFLD
FT	DIUPLFLD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	SEQUENCE
QO	326 AA; 37112 MW; 1261AA373596C00 CRC64;

[illegible]

Search completed: May 27, 2004, 15:45:16
Job time : 10.5 secs

Query Match	8.3%	Score 153.5;	DB 1;	Length 326;
Best Local Similarity	27.7%;	Pred. No. 3.2e-05;		
Matches 56;	Conservative 28;	Mismatches 81;	Indels 37;	Gaps 9;